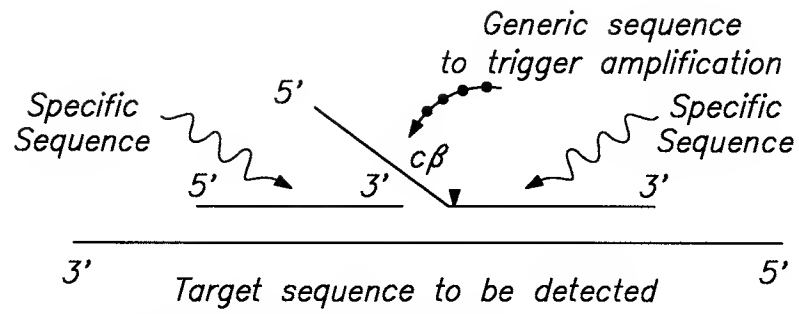
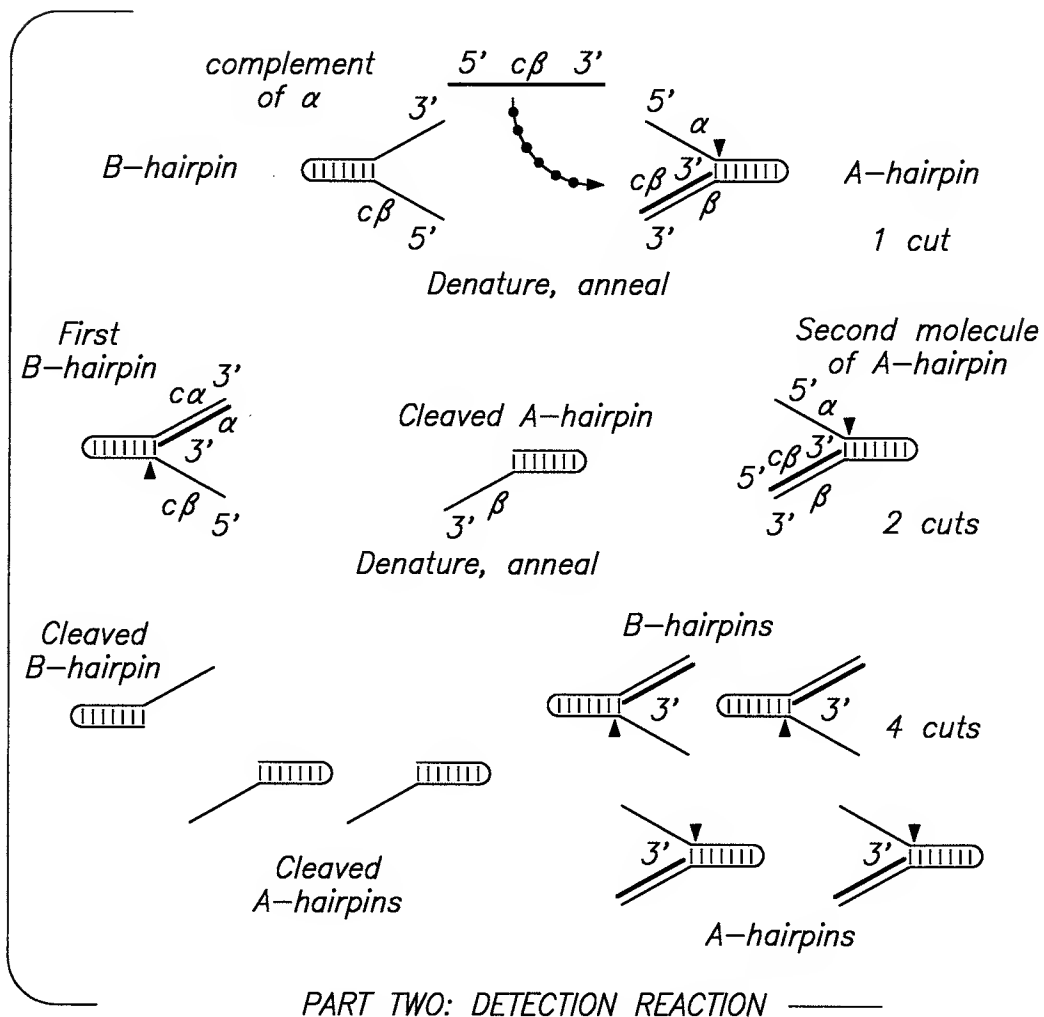
**FIG. 1A**

**FIG. 1B****PART ONE: TRIGGER REACTION****PART TWO: DETECTION REACTION**

## FIGURE 2

```

MAJORITY  CGAGGCGGACGACGTXCTGGCCACCCTGGCCAAGAGCGGAAAGGAGGGGTACGAGGTGCGCATCCTC
DNAPTAQ   :.....C.....G.....C.....C..... 417
DNAPTFL   T.....G.....CG..... 414
DNAPTTH   :.....T..C..... 420

MAJORITY  ACCGCCGACCGGACCTCTACCAGCTCCTTTCCGACCGCATCGCCGTCCTCCACCCCGAGGGGTACCTCA
DNAPTAQ   :.....AAA.....T.....CA..... 487
DNAPTFL   :..T.....G..G.....A.....T.....G.. 484
DNAPTTH   :.....A..G.C.....G.....CC..... 490

MAJORITY  TCACCCCGCGGTGGCTTTGGGAGAGTACGGCCTGAGGCCGGAGCAGTGGTGGACTACCGGGCCCTGGC
DNAPTAQ   :.....C.....A.....C..C.....CC.....A.. 557
DNAPTFL   :.....AC.....C.C.....T..C.....C..T 554
DNAPTTH   :.....A.....C.....T..C.....C..T 560

MAJORITY  GGGGGACCCCTCCGACAACCTCCCCGGGTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG
DNAPTAQ   C.....GAG.....T.....G..GAG.....T..GG.. 627
DNAPTFL   :.....G..T..A.....G.....A..G....A..CGC 624
DNAPTTH   :.....GAG.....T.....G.....TC.....A.. 630

MAJORITY  GAGTGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGTGAAGCCCGC...CXTCCGGGAGAAGA
DNAPTAQ   :.....GC.....C.....A..... 694
DNAPTFL   :.....T..C..C.....A.....T.....T.G.....C 691
DNAPTTH   :.....A.....A.....A.AAAA.G..... 700

```

FIGURE 2 (cont.)

MAJORITY TCCAGGCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCAGGTGCGCACCCGACCTGCCCTGCTGGA  
 DNAPTAQ ...T... ..C..T...A... ..C..GG..A... .. .. 764  
 DNAPTFL ...GGG... ..G.C...GCC..T...C..A... ..T... ..A...T... .. 761  
 DNAPTTH ..A... ..C...A... ..C.G... ..T... ..C... ..G... ..C... .. 770  
 MAJORITY GGTGGACTTCGCCAAGXGGCGGGAGCCCGACCGGGAGGGGCTTAGGGCCTTTCTGGAGAGGCTGGAGTTT  
 DNAPTAQ ... ..AA... .. ..A... .. .. ..T... .. 834  
 DNAPTFL ... ..GG.G.C.C..CACA...A... ..T... ..T..GC... ..T... ..C..T... .. 831  
 DNAPTTH ... ..C... ..C..G... .. .. .. ..C... .. ..C... .. 840  
 MAJORITY GGCAGCCTCCTCCACGAGTTTCGGCCTCCTGGAGGGGCCCCAAGGCCCTGGAGGAGGCCCTGGCCCCCGC  
 DNAPTAQ ... .. .. ..T... ..AA... .. .. .. .. 904  
 DNAPTFL ..A... .. .. .. ..G..G... ..GGCA... .. ..T... .. 901  
 DNAPTTH ... .. .. .. ..C... ..GCCC... .. .. .. 910  
 MAJORITY CGGAAGGGGCTTCGTGGGCTTTGTCTCTTTCCCGCCCCGAGCCCCATGTGGGCCGAGCTTCTGGCCCTGGC  
 DNAPTAQ ... .. .. .. ..G... ..AAG... .. .. ..T... .. 974  
 DNAPTFL ... .. .. .. ..TC.T... .. .. ..T... .. .. .. 971  
 DNAPTTH ... .. .. .. ..C... ..C... .. .. ..G... ..AAA... .. 980  
 MAJORITY CGCCGCCAGGGGGCCGGGTCCACCGGGCACCAAGACCCCTTTAXGGGCCTXAGGGACCTXAAGGAGGTG  
 DNAPTAQ ... .. .. .. ..G... .. .. ..C..C..G..T.A..AA.C... ..C... ..G... ..C... .. 1044  
 DNAPTFL T.GG..GT... .. ..G..CC... ..T... .. ..A... .. ..C... ..G... .. ..T... ..G... .. 1041  
 DNAPTTH ... ..TG... .. ..C... .. ..G... .. .. ..G... ..G.C... ..G..A.A... ..C... .. 1050

FIGURE 2 (cont.)

```

MAJORITY  CGGGGXCTCCTCGCCAAGGACCTGGCCGTTTTGGCCCTGAGGGAGGGCCTXGACCTCXTGCCCCGGGGACG

DNAPTAQ   .....G..T.....A.....AG.....C.....A.....T.G....CC.....C.... 1114
DNAPTFL   ....AA.....G.....G.....C.....G.....T.C..A.A..... 1111
DNAPTTH   .....C.....C.....TC.....G.A.....G.....G..... 1120

MAJORITY  ACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACCACCCCGAGGGGTGGCCCCGGCGCTACGG

DNAPTAQ   .....G.....T.....T.....T.....T.....T.....T..... 1184
DNAPTFL   .....G.....T.....T.....T.....T.....T.....T..... 1181
DNAPTTH   .....G.....T.....T.....T.....T.....T.....T..... 1190

MAJORITY  GGGGGAGTGGACGGAGGAXGCGGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGAG

DNAPTAQ   C.....G.....G.....GC.....T.....GC.....GCC.....GTG..G. 1254
DNAPTFL   .....T.....A.....GG.....C.C.....A..C...AAA.... 1260
DNAPTTH   .....C..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260

MAJORITY  CGCCTTGAGGGGAGGAGGCTCCTTTGGCTTTACCAGGAGGTGGAGAAGCCCCCTTTCCCGGGTCCIGG

DNAPTAQ   A.G.....A.....G.....G.....G.....GCT.....GCT..... 1324
DNAPTFL   .....A...A..A..AC.C.G.....G.....G.....G.....GT... 1321
DNAPTTH   .....C.....A.....C.....C.....A.....C.....C..... 1330

MAJORITY  CCCACATGGAGGCCACGGGGGTXCGGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA

DNAPTAQ   .....G.....G..C.....T...AG....T.G.....C... 1394
DNAPTFL   ...GG.....C.....C.....C.....A..C 1391
DNAPTTH   .....C.....A.....T.....T.....C.T..... 1400

```

FIGURE 2 (cont.)

```

MAJORITY  GGAGATCCGCCCTCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGAC
DNAPTAQ    .....GC.....CC..... 1464
DNAPTFL    .....G.G....AG..G.....C... 1461
DNAPTTH    .....T.....G..... 1470

MAJORITY  CAGCTGGAAAGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC
DNAPTAQ    .....C.....A.....C..... 1534
DNAPTFL    .....GC.....G.C..G..T.....G..G..A. 1531
DNAPTTH    .....TA.....T.G..G.....C.A.....A..... 1540

MAJORITY  GCTCCACGAGCGCCGCTGCTGGAGGCCCTXCGXGAGGGCCCAACCCCATCTCGTGGAGAAGATCCTGCAGTA
DNAPTAQ    .....C.....C..C..... 1604
DNAPTFL    .....T.....G..A.....CCGC..... 1601
DNAPTTH    .....G.....A..G.....C...C. 1610

MAJORITY  CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCTGCCCXGXCCCTCGTCCACCCAGGACGGGC
DNAPTAQ    .....G...G.....T.....G.A...A..... 1674
DNAPTFL    .....A.....C.C...G.....A...C... 1671
DNAPTTH    .....G.G.....AAG.....G..... 1680

MAJORITY  CGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTTAGTAGCTCCGACCCCAACCTGC
DNAPTAQ    .....A.....A.....T.....C. 1744
DNAPTFL    .....G.....C.....TCC..... 1741
DNAPTTH    .....G.....G..... 1750

```

FIGURE 2 (cont.)

```

MAJORITY AGAACATCCCCGTCCGCACCCXCTGGGCCAGAGGATCCGCCCGGGCCCTTCGTGGCCGAGGAGGGXTGGGT

DNAPTAQ .....G..T..G.....A.C.....G...C. 1814
DNAPTFL .....G.....T.....C.C.....A.....C..... 1811
DNAPTTH .....CT.....C.....T.....C..... 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTCTGGCCACCTCTCCGGGGACGAGAACCTG

DNAPTAQ A.....T.T.....C.....A.....G.....C..... 1884
DNAPTFL .C.....T.T.....C.....T.....C..... 1881
DNAPTTH .....T.T.....C.....T.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCCAGGAGGGGAGGACATCCACACCCAGACCGCCAGCTGGATGTTCCGGCGTCCCCCCCCG

DNAPTAQ .....T.....C.....C.....GG.....G.....G... 1954
DNAPTFL .....T.....T.....T.....TT.....C. 1951
DNAPTTH .....A.....A.....A.....A..... 1960

MAJORITY AGGCCGTGGACCCCTGATGCGCCCGGGCGCCAGACCATCAACTTCGGGGTCCTCTACGGCATGTCCGC

DNAPTAQ .....T.....G.....G... 2024
DNAPTFL .A.GG..A.....T.....G.....G..... 2021
DNAPTTH .....GG.G.....C.....C..... 2030

MAJORITY CCACCGCCTCTCCCAGGAGCTTGCCCATCCCCCTACGAGGAGGGCGGTGGCCTTCATTGAGCGCTACTTCCAG

DNAPTAQ .....A.....T.....CCA.....T... 2094
DNAPTFL .....GG.....T..... 2091
DNAPTTH ...TA.G.....T.A.....A 2100

```

FIGURE 2 (cont.)



```

MAJORITY AGCTTCCCAAGGTGCGGGCCTGGATTGAGAAAGACCCTGGAGGAGGGCAGGAGCGGGGGGTACGTGGAGA
DNAPTAQ ..... 2164
DNAPTFL ...A.....GG.....C.....C.CC.....T..... 2161
DNAPTTH .....A.A.....G.....A.....C.....A. 2170

MAJORITY CCCTCTTCGGCCGCGGCTACGTGCCCCGACCTCAACGCCCGGTGAAGAGCGTGCGGGAGGGCGCGGA
DNAPTAQ .....C.....A.....AG.G.....C..... 2234
DNAPTFL .....T.....C.....C..... 2231
DNAPTTH .....AA.AA.....CA.....C..... 2240

MAJORITY GCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCCGACCTCATGAAGCTGGCCATGGTGAAGCTC
DNAPTAQ .....T..... 2304
DNAPTFL .....G.....CG...T 2301
DNAPTTH .....C..... 2310

MAJORITY TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCCACGACGAGCTGGTCTCGAGGCC
DNAPTAQ .....A...GG.....T..... 2374
DNAPTFL .....T.....C.....G.....TT.G.....G..... 2371
DNAPTTH .....C..C.G...G.....C.C.....C.....G..... 2380

MAJORITY CCAAAGAGCGGGCGGAGGXGGTGGCCGCTTTGGCCAAGGAGGTCTATCCCTCGGCCGT
DNAPTAQ .....A.....A.....CC.....CGGC.....G..... 2444
DNAPTFL .....G..C.....AG..A.....GG.....CAG.. 2441
DNAPTTH .....C...C.....C.....A.....C.....C..... 2450

```

FIGURE 2 (cont.)

MAJORITY	GCCCCCTGGAGGTGGAGGTGGGGATGGGGGGAGGACTGGCTCTCCGCCCAAGGAGTAG	
DNAPTAQ	.....A.....GA	2499
DNAPTFL	.....CC.....	2496
DNAPTTH	.....T.....GT...	2505

FIGURE 2 (cont.)

```

MAJORITY MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPVQAVYGFAKSLLKALKEDG·DAVXVVVFDK
TAQ PRO  .RG.....H.....I.....69
TFL PRO  .V.....V.....68
TTH PRO  .E.....YK..F.....70

MAJORITY APSFRHEAYEAYKAGRAPTPEDFPROLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL
TAQ PRO  .GG.....A.....S.....139
TFL PRO  .V.....F.....R.....138
TTH PRO  .FT.....140

MAJORITY TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDSNLPGVKGIGECTAXKLLX
TAQ PRO  .K.....H.....D..A...T..E.....R...E 209
TFL PRO  .E...I.....Y.....A.....I.....QR..IR 208
TTH PRO  .V...V.....H...E...F...V.....L...K 210

MAJORITY EWGSLLENLLKNLDRVKP·XXREKIXAHMEDLXLSSXXLSXVRTDLPLEVDVFAXRREPDRGLRAFLERLEF
TAQ PRO  .A.....L...AI...L...D..K..WD.AK.....K.....R.....278
TFL PRO  .FQH...Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....277
TTH PRO  .ENV.....K..L...R..LE..R.....L.QG.....280

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEALLALAAARXGRVHRAXDPLXGLRDLKEV
TAQ PRO  .S.....K.....D.....PE.YKA.....A 348
TFL PRO  .G..A.....L..SF.....G.WE..L...Q...R.....G.. 347
TTH PRO  .A.AP.....K.....C.D.....A...A..K..... 350

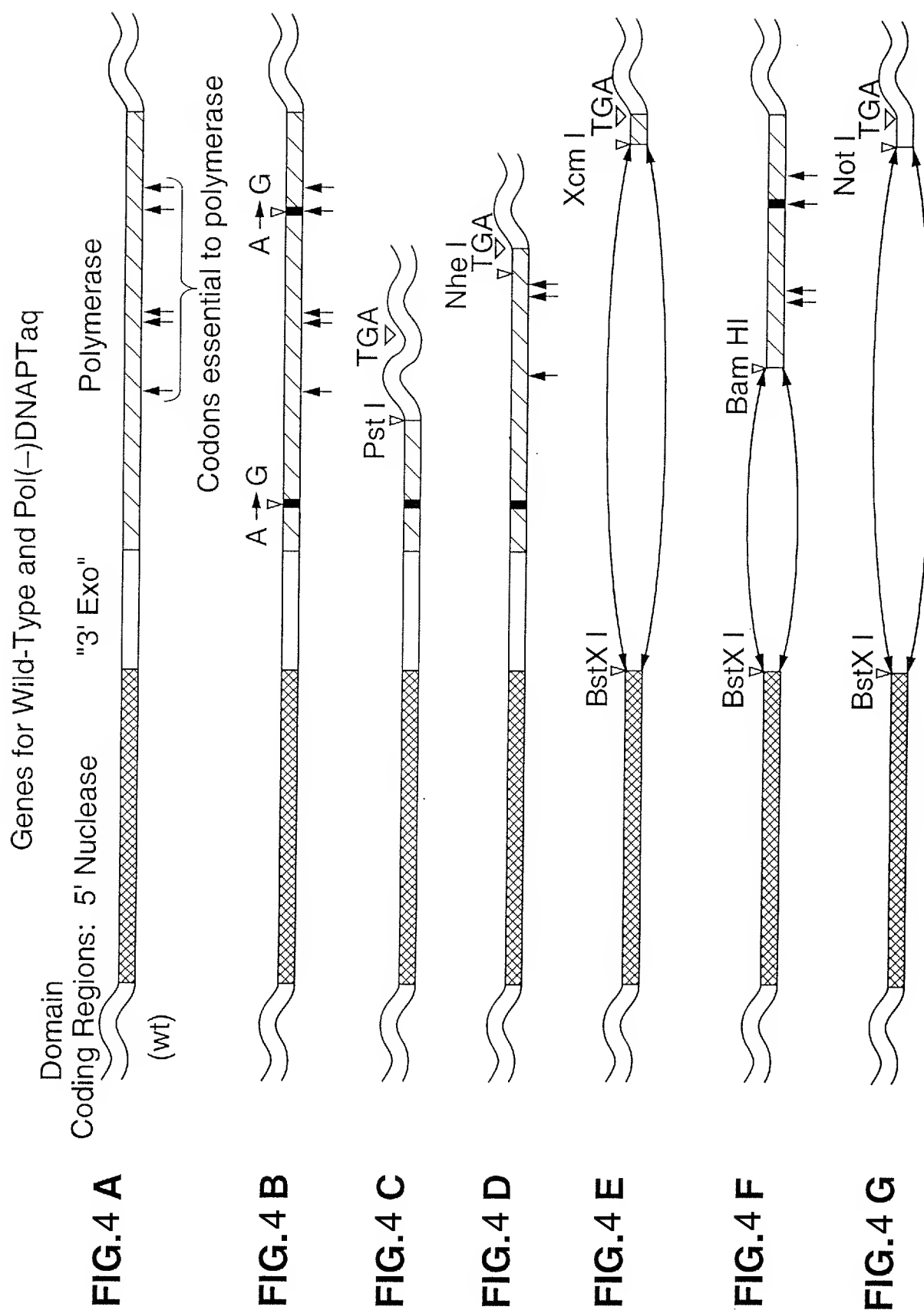
```

FIGURE 3

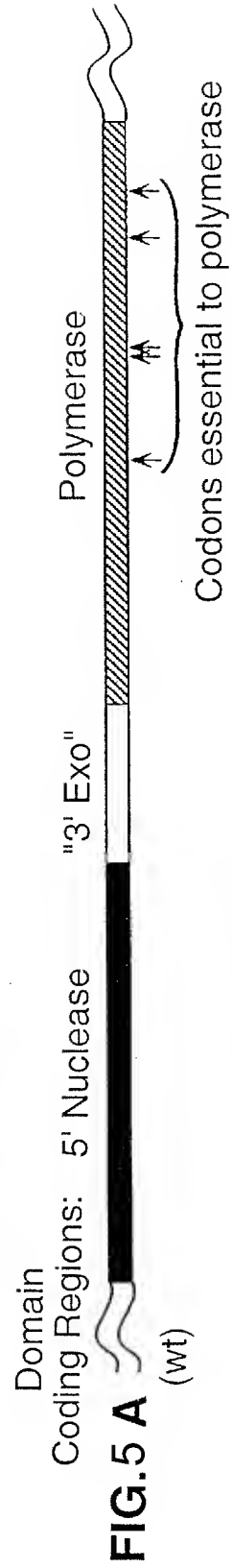
MAJORITY		RGLLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEAGEDERALLSERLFXNLXX	
TAQ	PRO	.....S.....G.P.....E.....A.....A.....WG	418
TFL	PRO	..I.....F.E.....A.....QT.KE	417
TTH	PRO	.....S.....V.....AH.....HR..LK	420
MAJORITY		RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRLEEVEFRLAGHPFNLSRD	
TAQ	PRO	.....R.....R.....A.....R.....A.....A.....	488
TFL	PRO	..K.....E.....R.....EA.V.Q.....	487
TTH	PRO	.....K.....H.....L.....	490
MAJORITY		QLERVLFDELGLPAIGKTEKTKRSTSAAVLEALREAHPIVEKILQYRELTKLKNITYIDPLPXLVHPRTG	
TAQ	PRO	.....R.....L.....Q.....I.....S.....D.I.....	558
TFL	PRO	.....R.....L.....Q.....DR.....A.....K.....	557
TTH	PRO	.....R.....L.....Q.....H.....V.....S.....	560
MAJORITY		RLHTRFNQTATATGRLSSSDPNLQNIQIPVTRPLGQIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL	
TAQ	PRO	.....I.....L.....	628
TFL	PRO	.....V.....V.....	627
TTH	PRO	.....A.....A.....	630
MAJORITY		IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAVAFIERYFQ	
TAQ	PRO	.....E.....R.....Q.....	698
TFL	PRO	.....S.....G.....S.....	697
TTH	PRO	.....K.....V.....	700

FIGURE 3 (cont.)

FIGURE 3 (cont.)



## Genes for Wild-Type and Pol(-)DNAPTfl



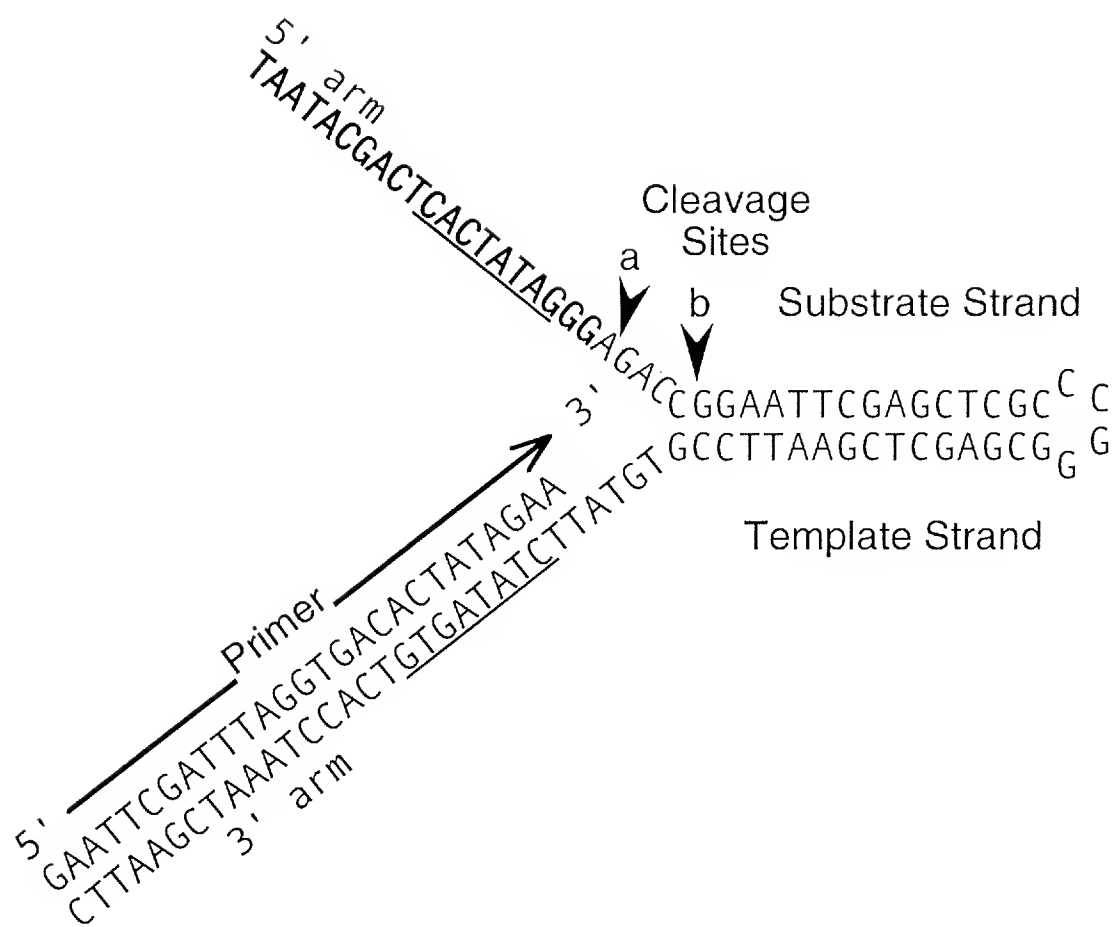


FIGURE 6



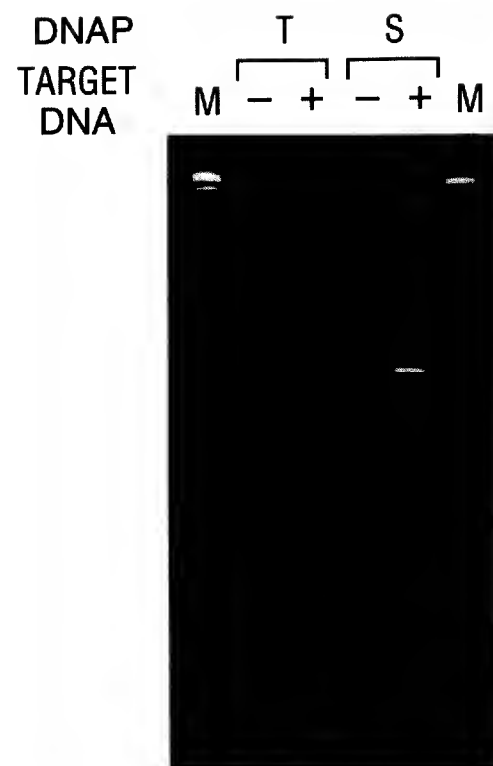


FIGURE 7

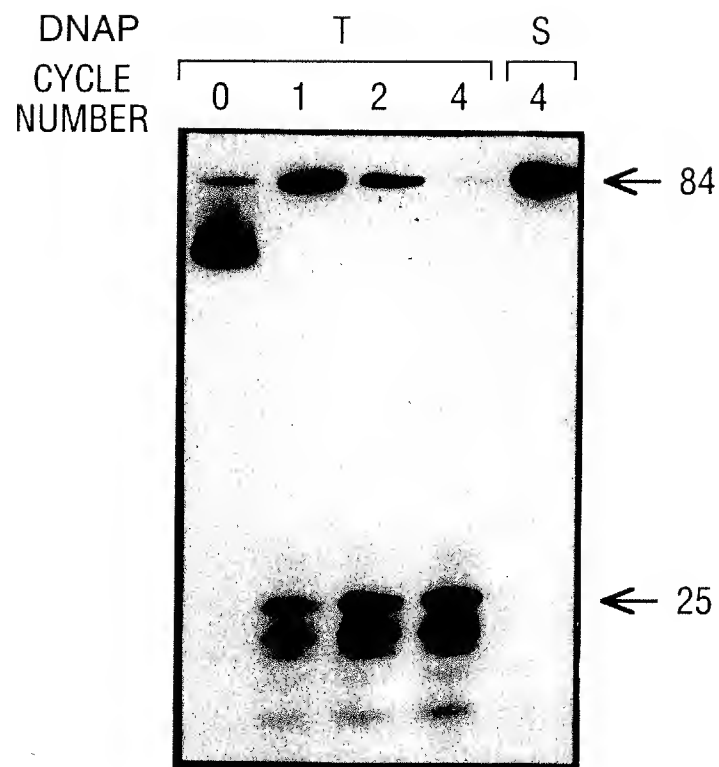
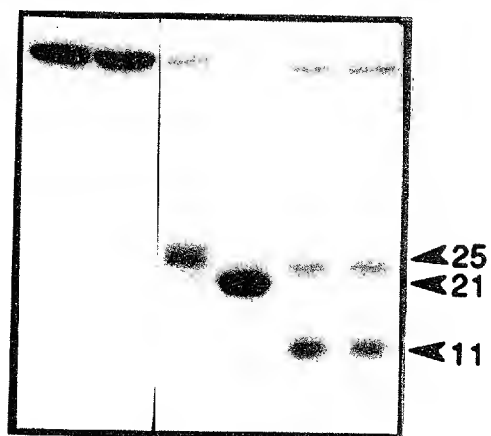
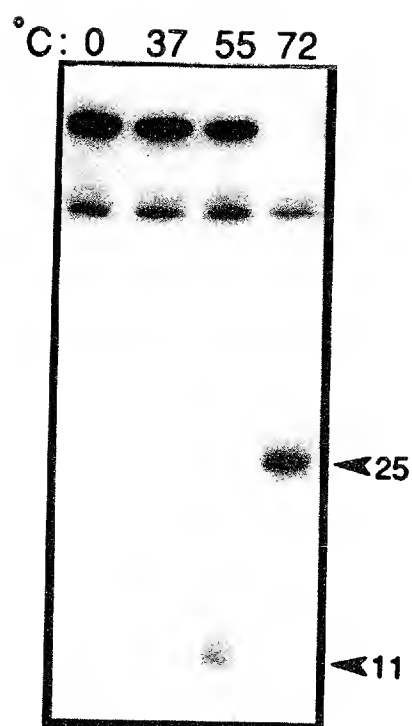


FIGURE 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

**FIG. 9A****FIG. 9B**

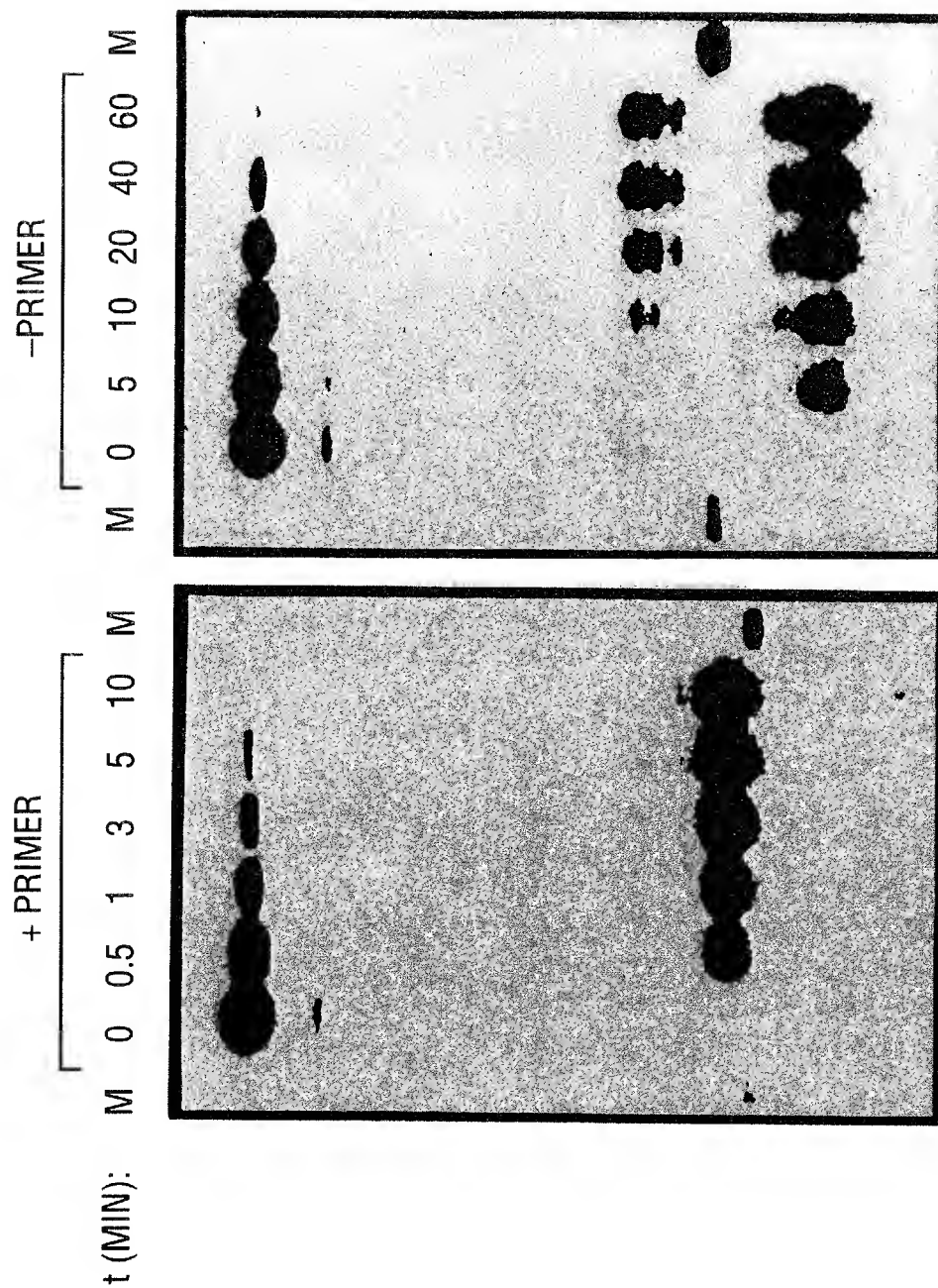


FIG. 10A

FIG. 10B

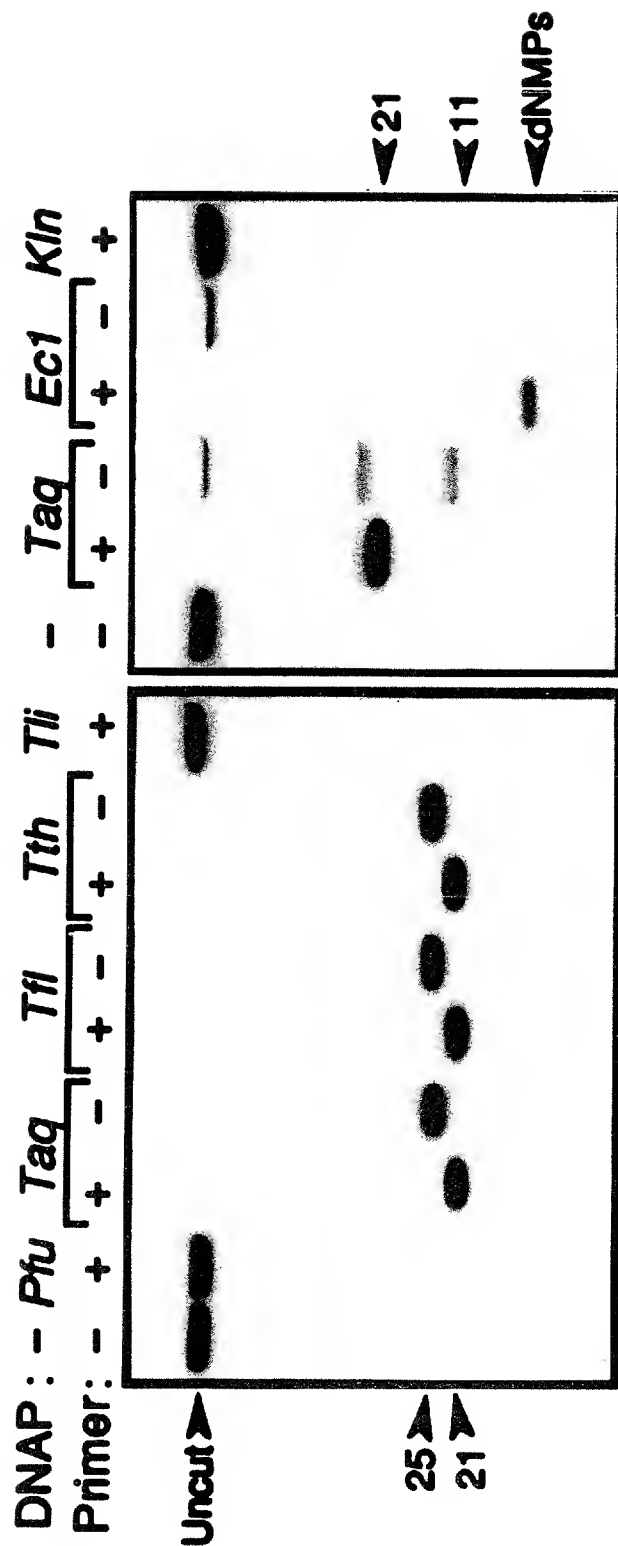


FIG. 11A

FIG. 11B

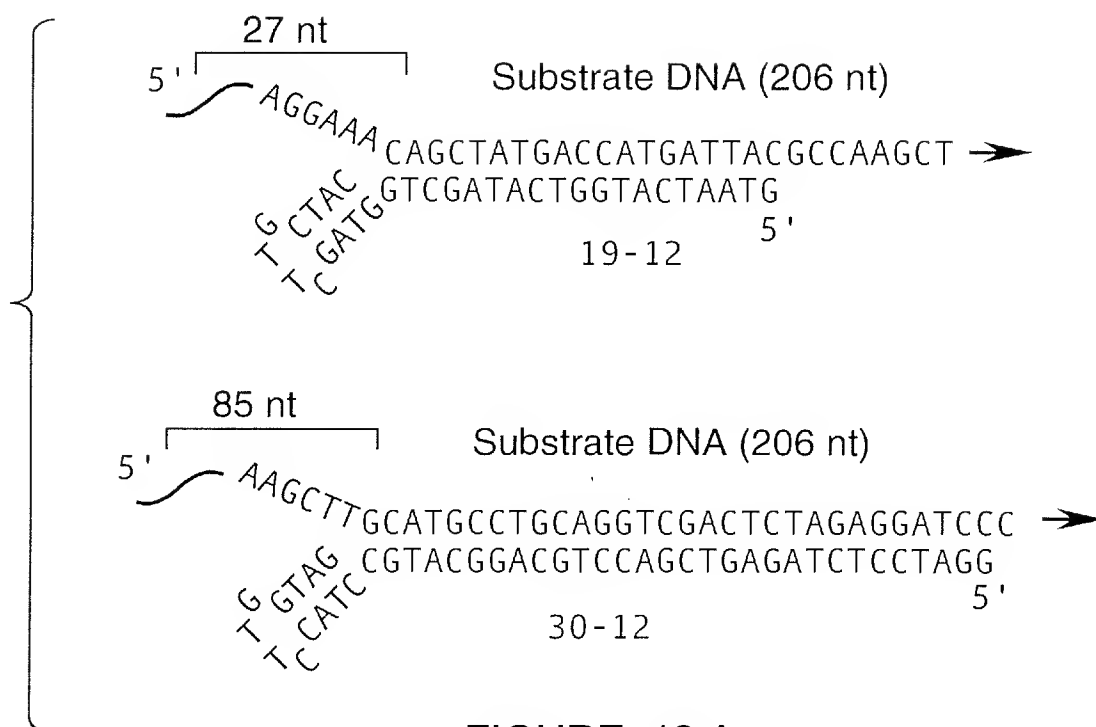


FIGURE 12 A

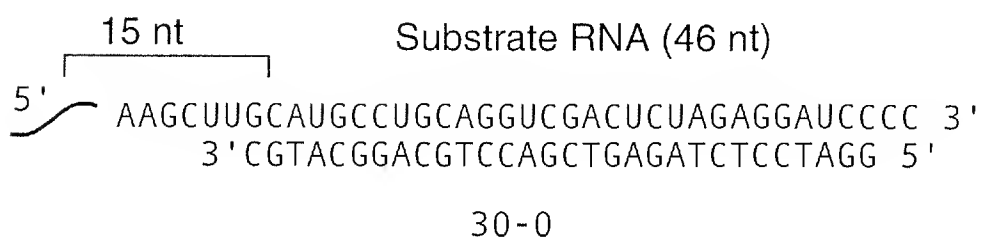


FIGURE 13 A

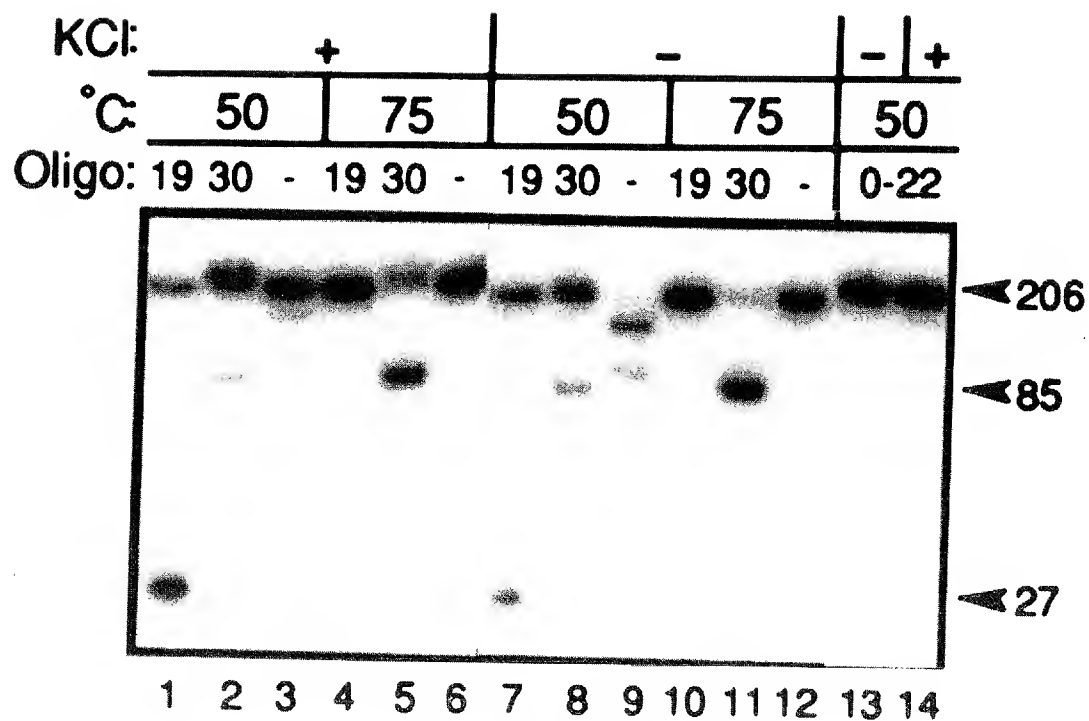


FIG. 12B

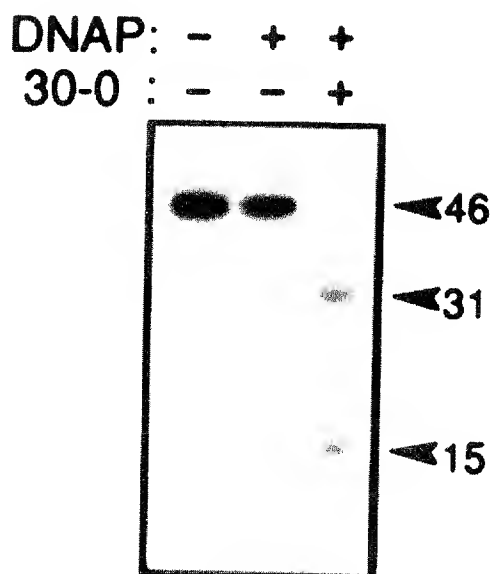
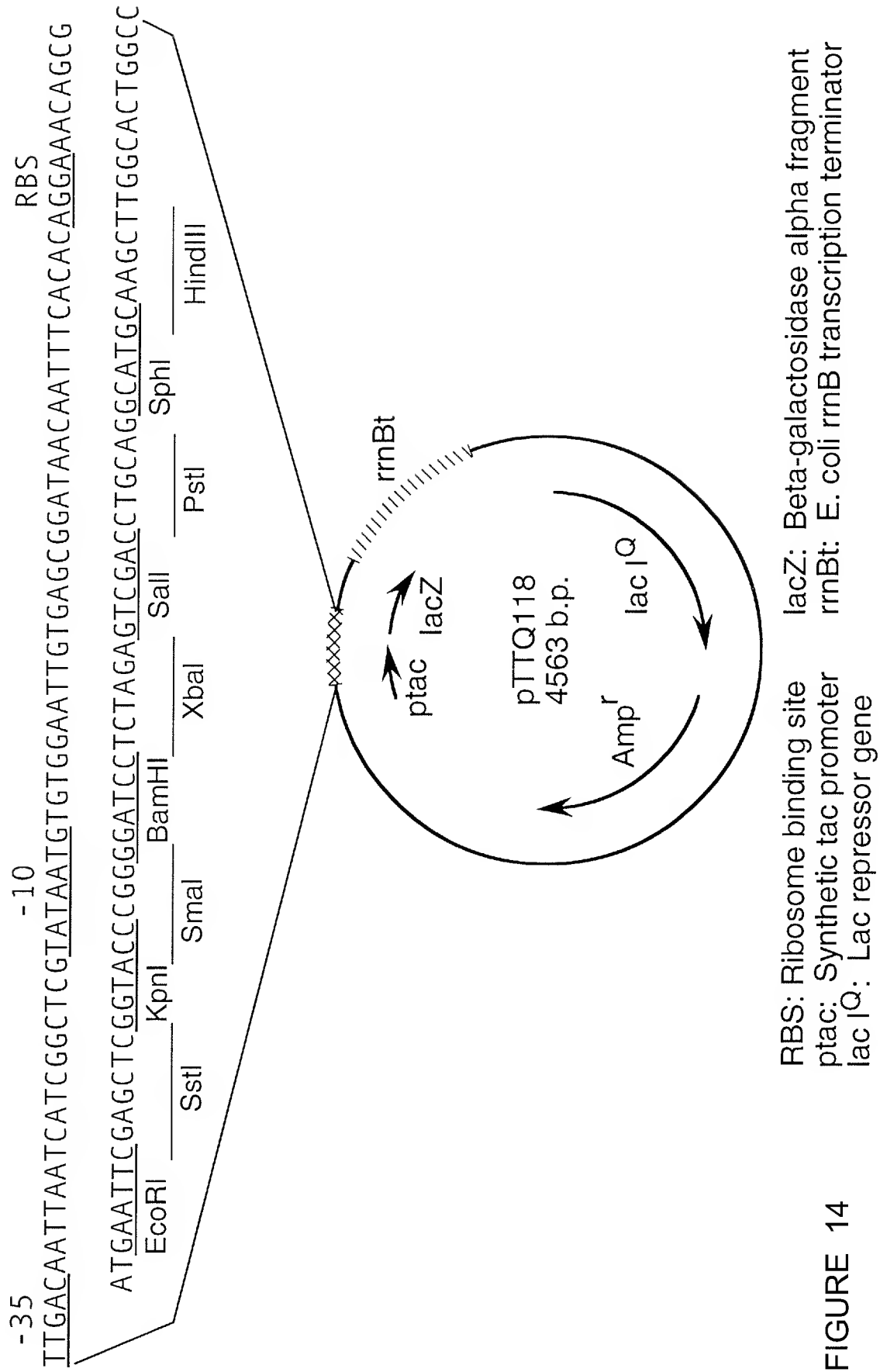
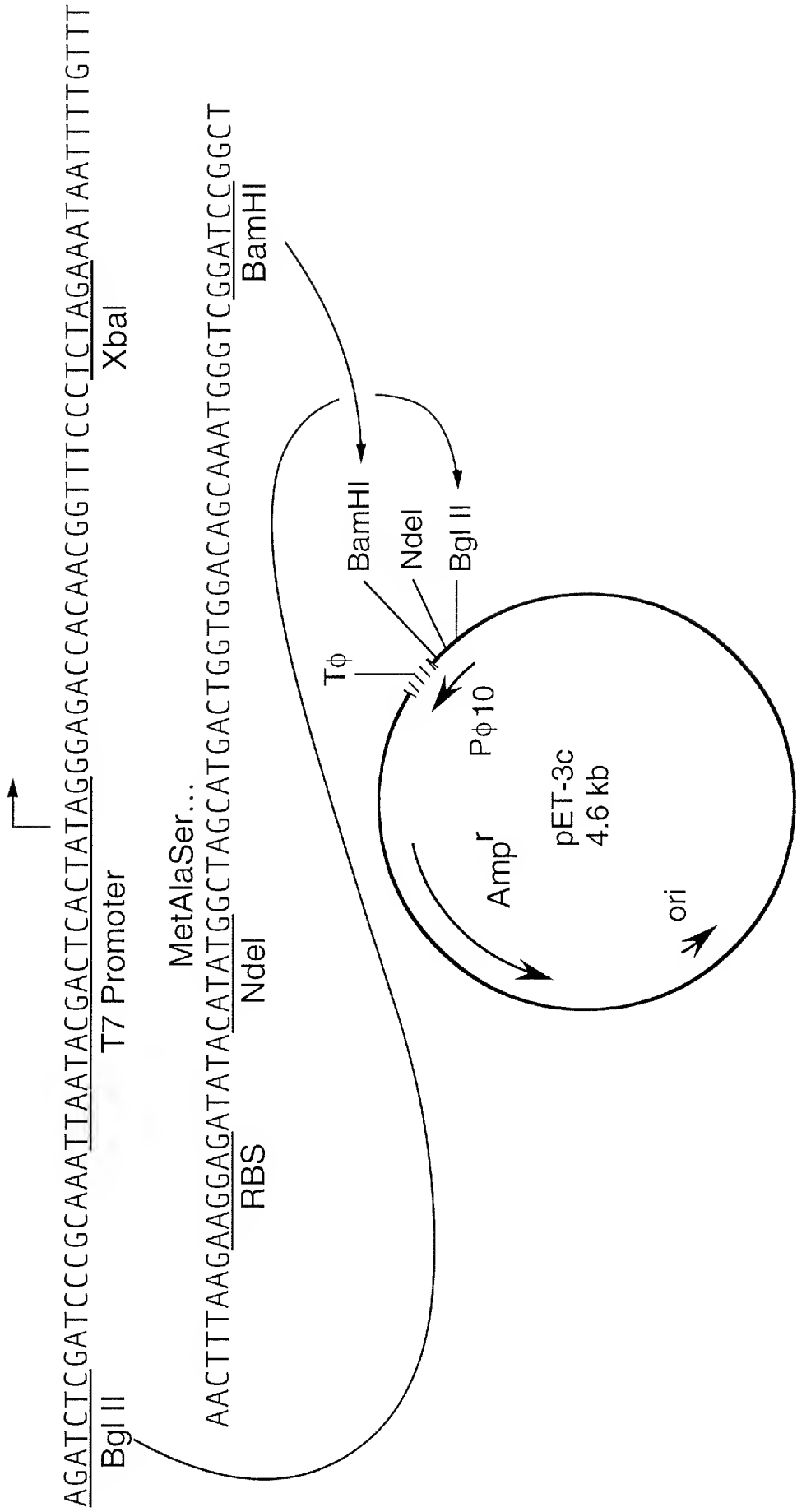


FIG. 13B



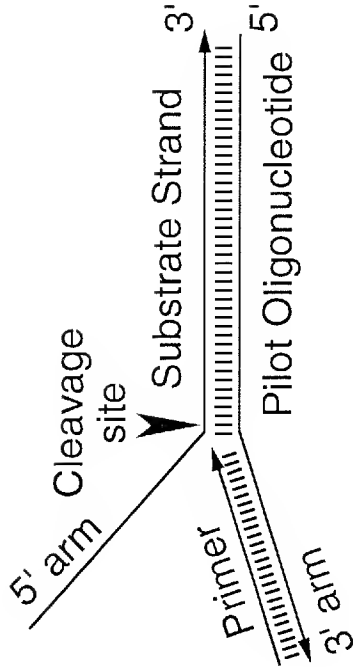
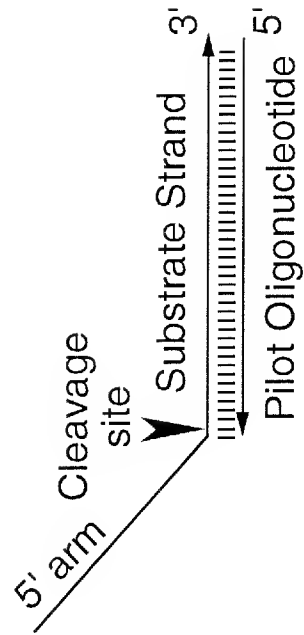
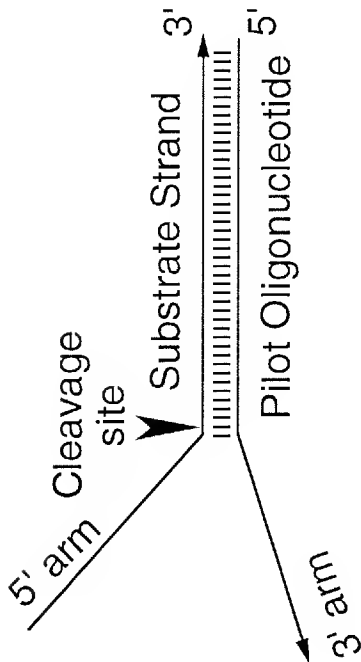
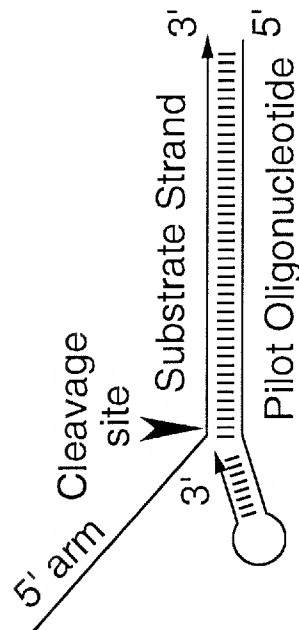
RBS: Ribosome binding site  
ptac: Synthetic tac promoter  
lac I<sup>Q</sup>: Lac repressor gene  
lacZ: Beta-galactosidase alpha fragment  
rrnBt: E. coli rrnB transcription terminator





P<sub>φ10</sub>: Bacteriophage T7  $\phi$ 10 promoter      RBS: Ribosome binding site  
T<sub>φ</sub>: T7  $\phi$  Terminator

FIGURE 15

**FIG. 16B****FIG. 16D****FIG. 16A****FIG. 16C**

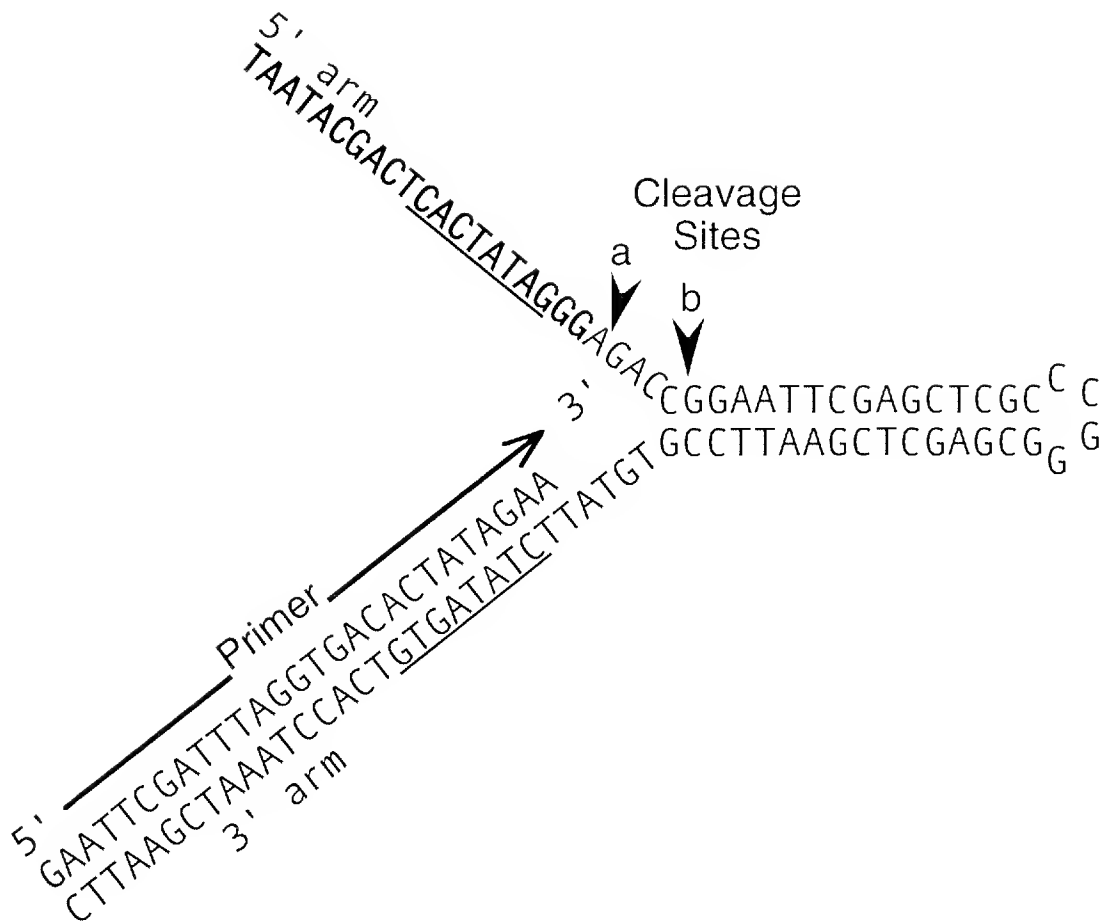
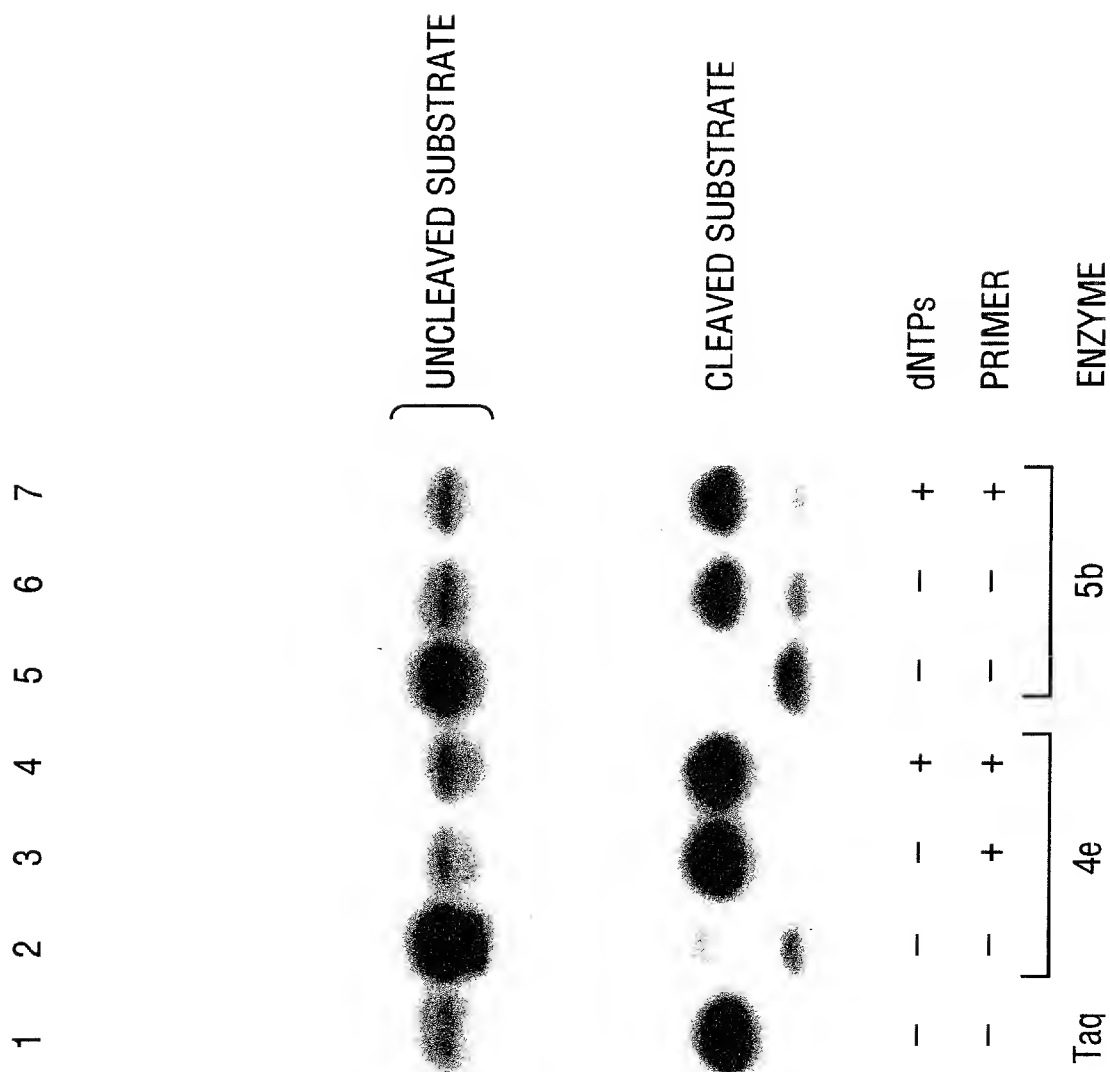
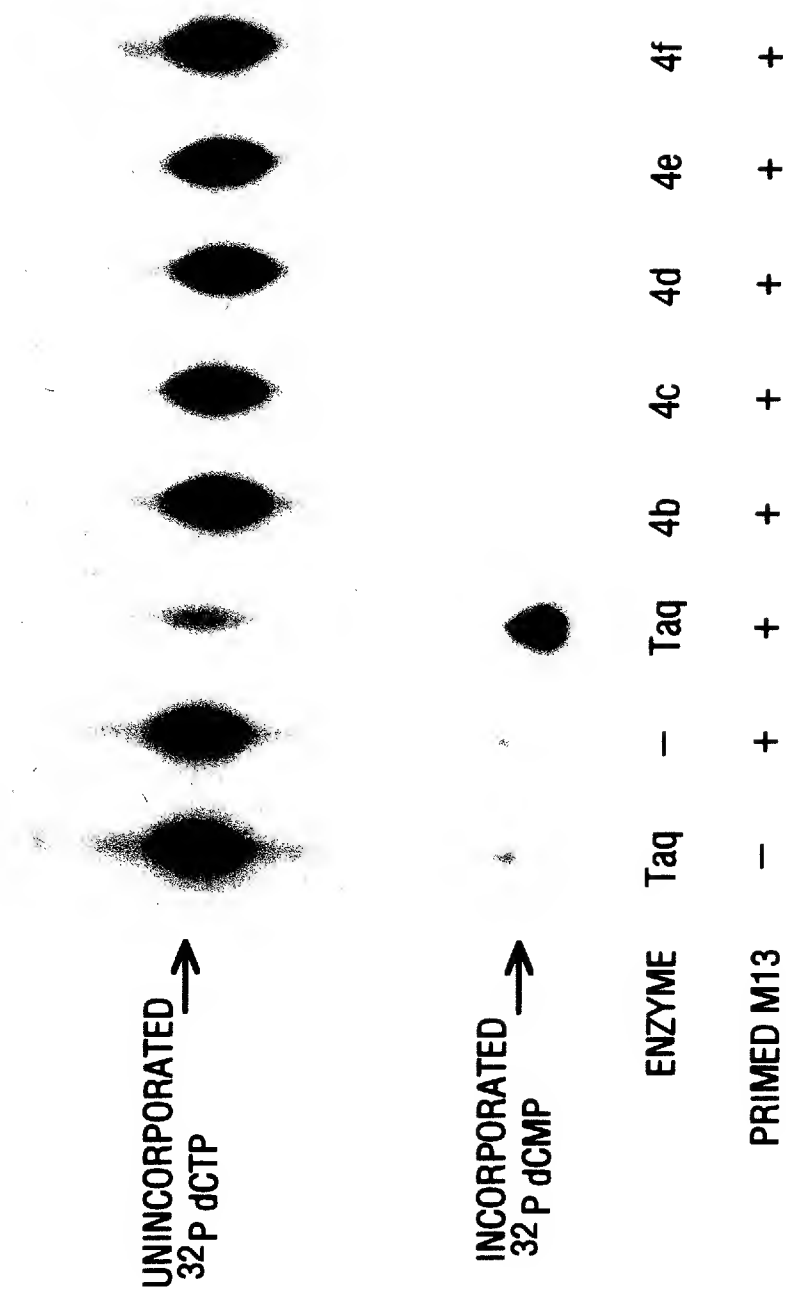


FIGURE 16 E



**FIG. 17**



**FIG. 18**

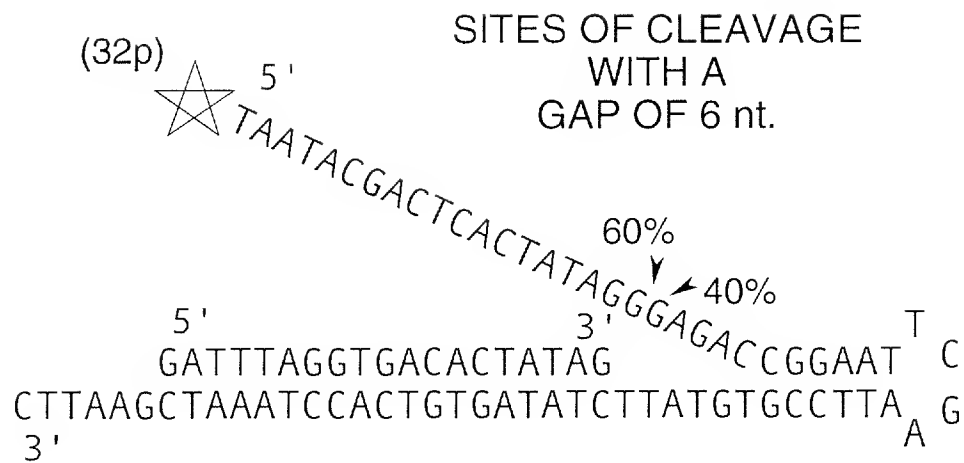
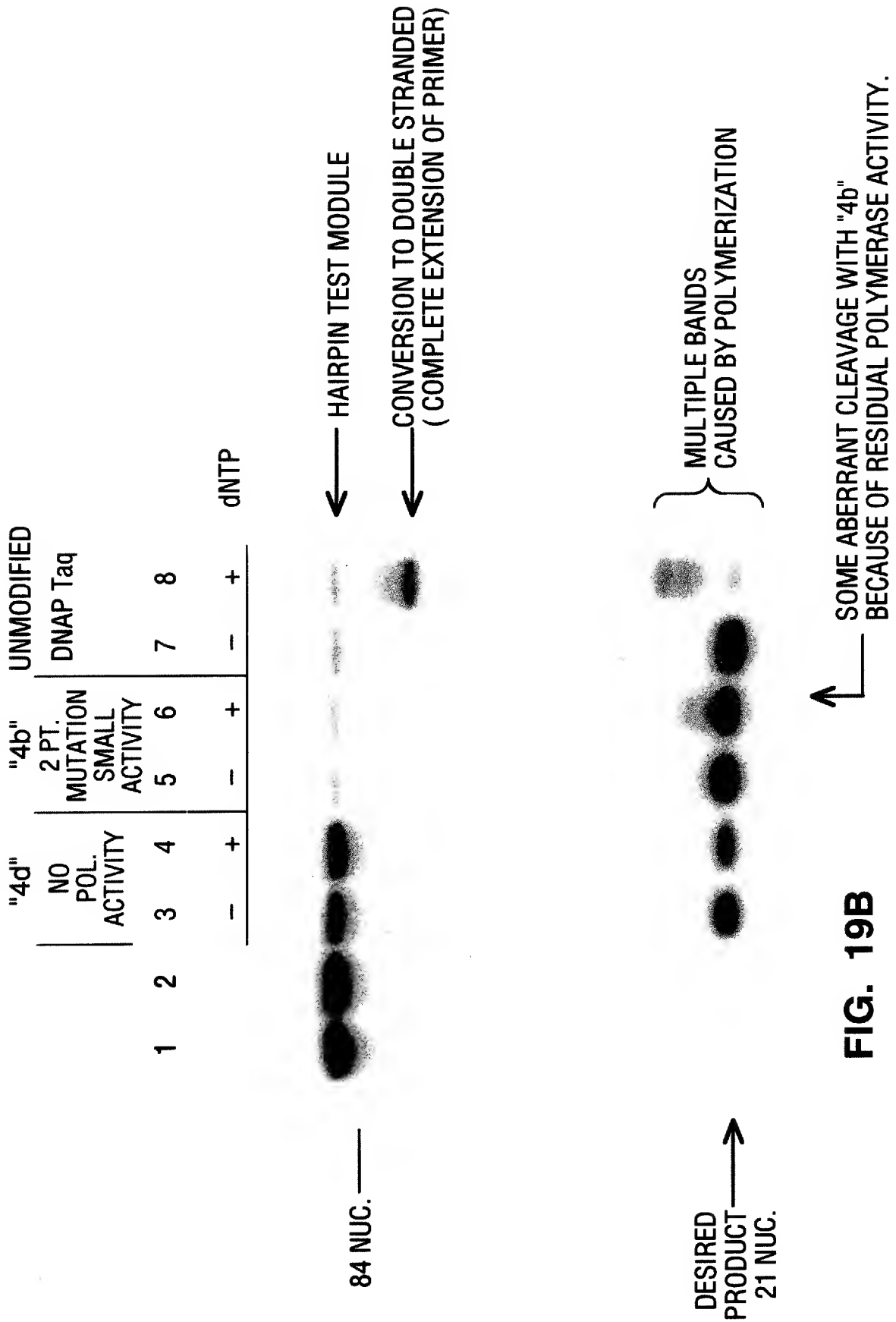


FIGURE 19 A



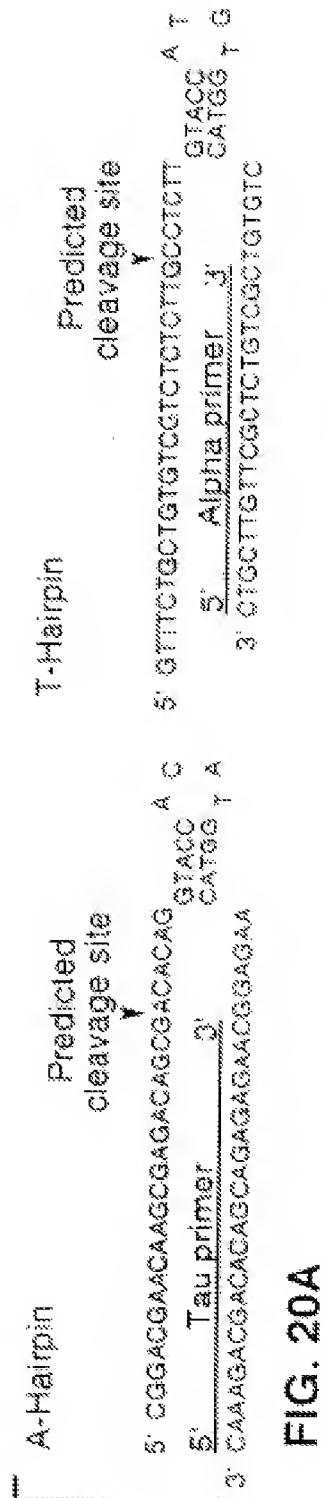


FIG. 20A

Sequence of alpha primer:

5' GACGACACGCGACGACG 3'

2008

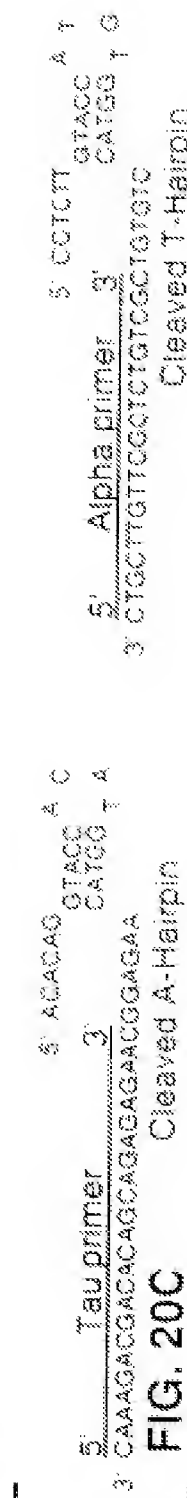


FIG. 20C

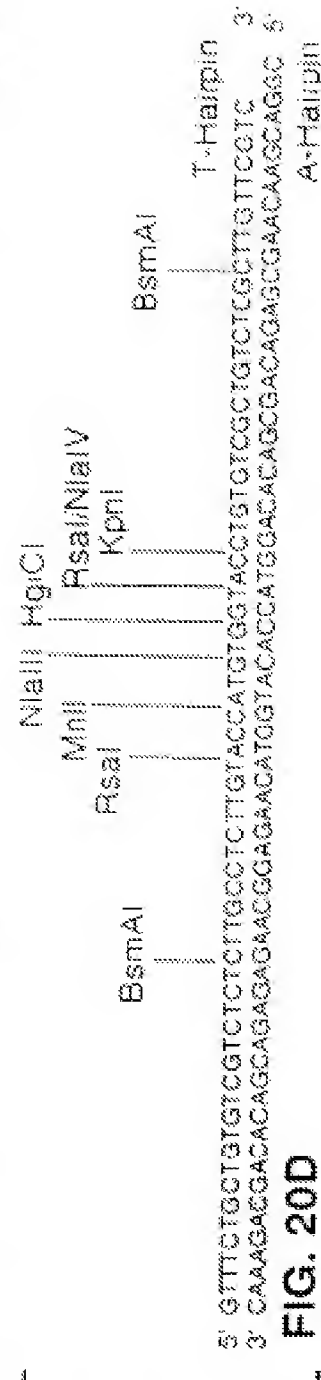


FIG. 20D



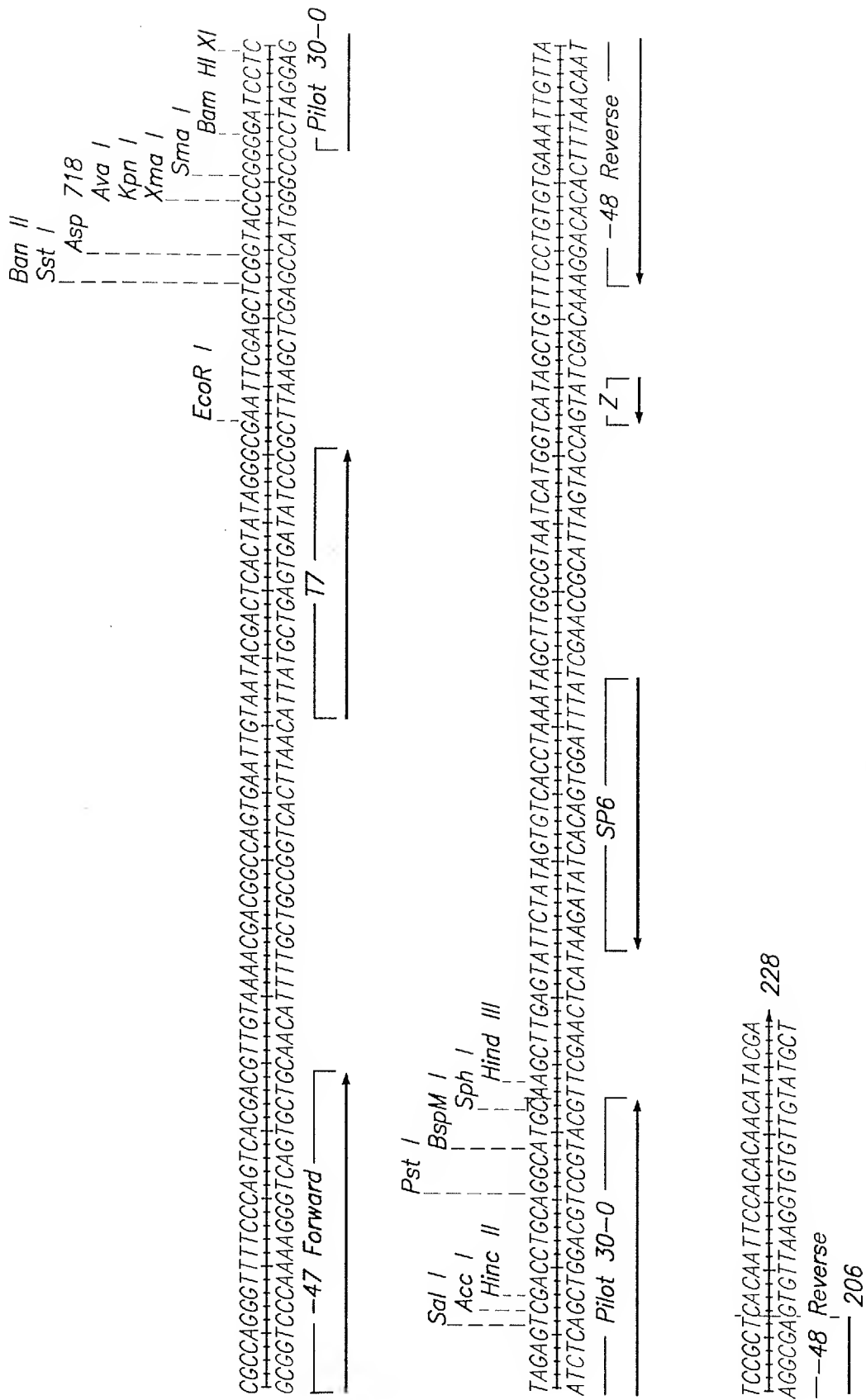


FIGURE 21

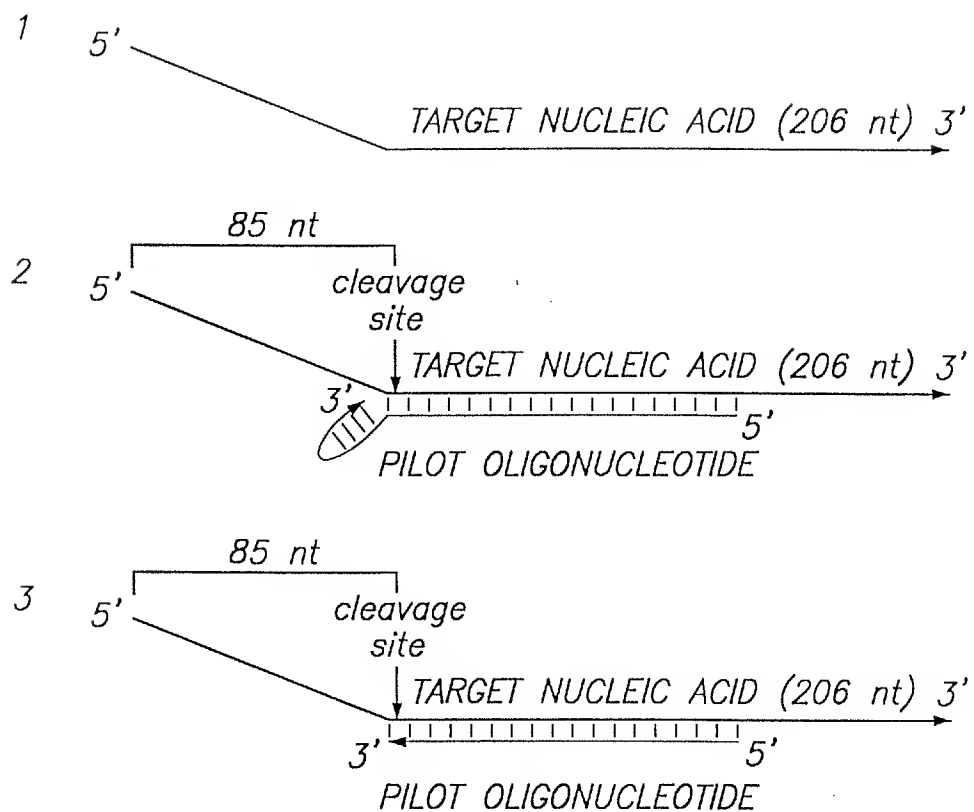


FIGURE 22 A

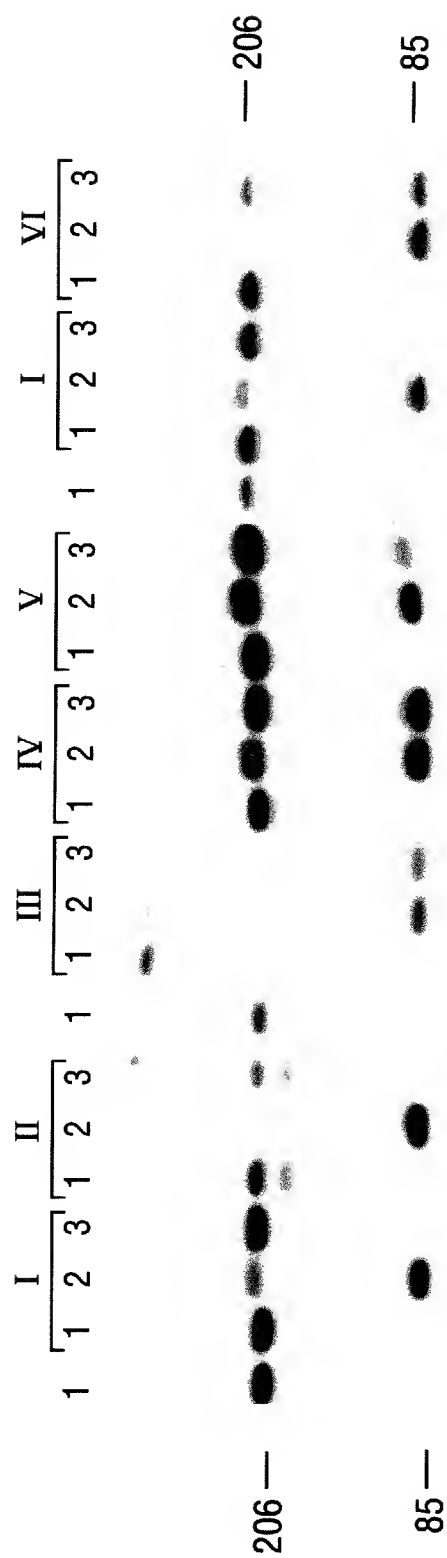
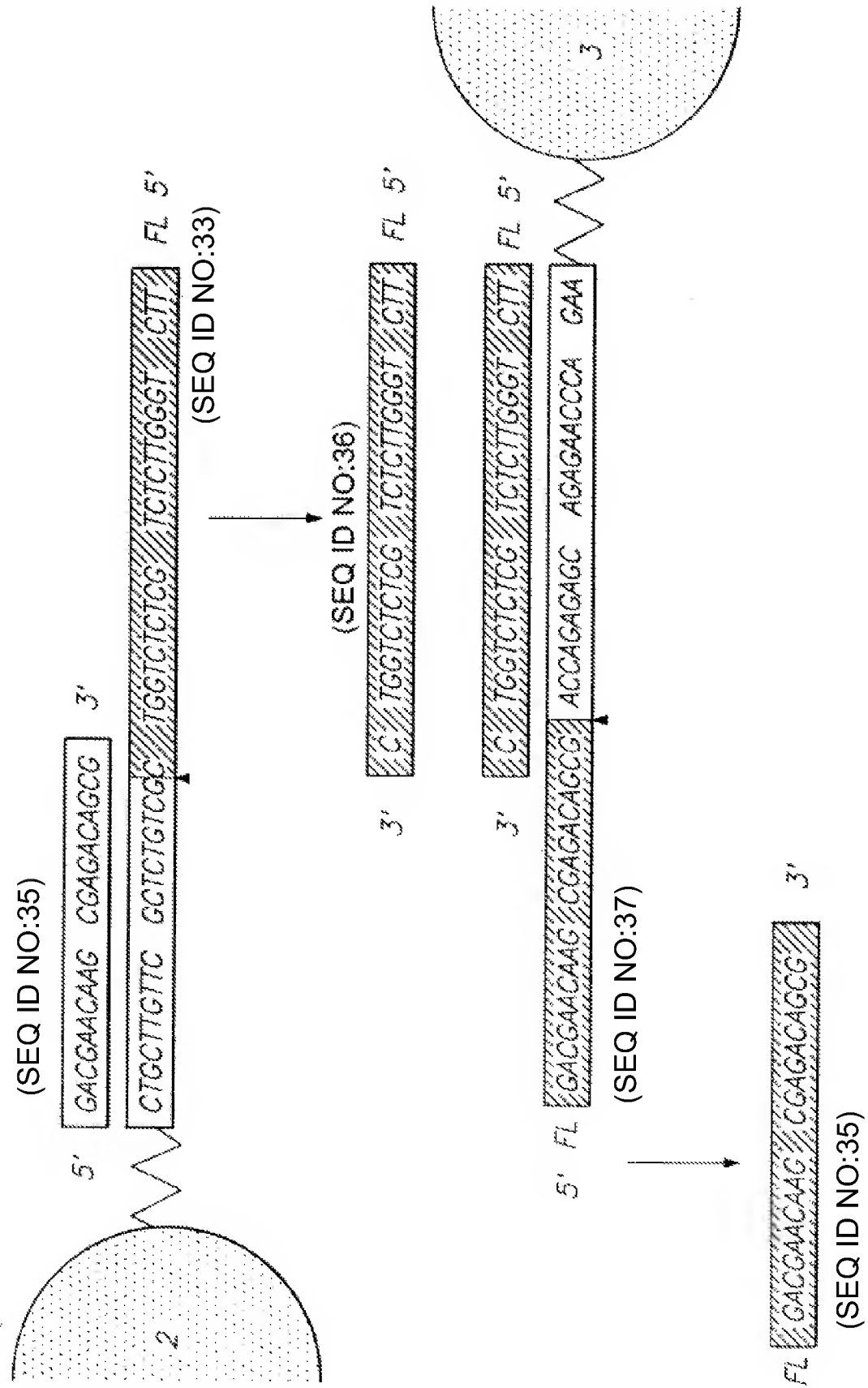


FIG. 22B

FIGURE 23



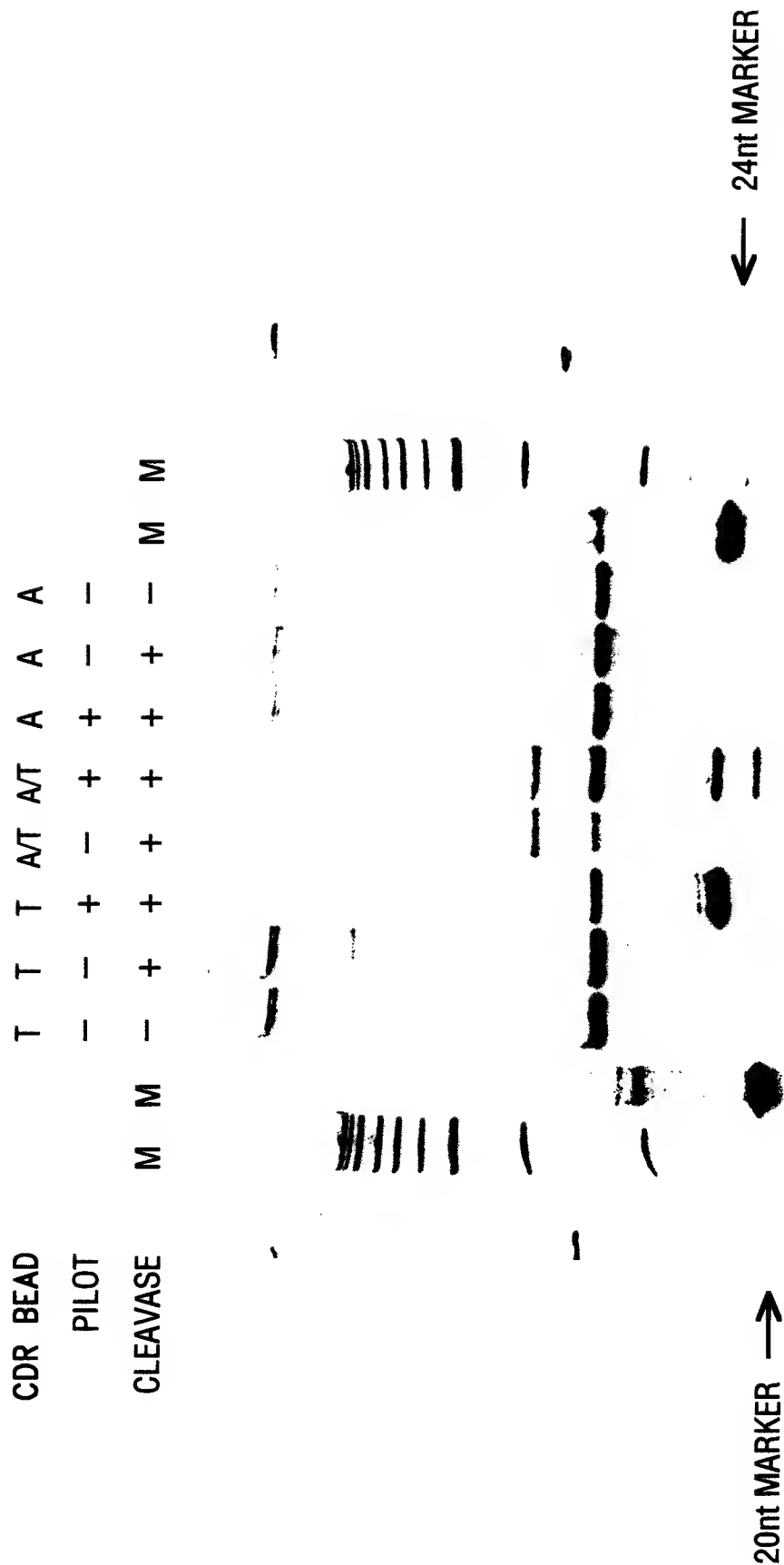


FIG. 24

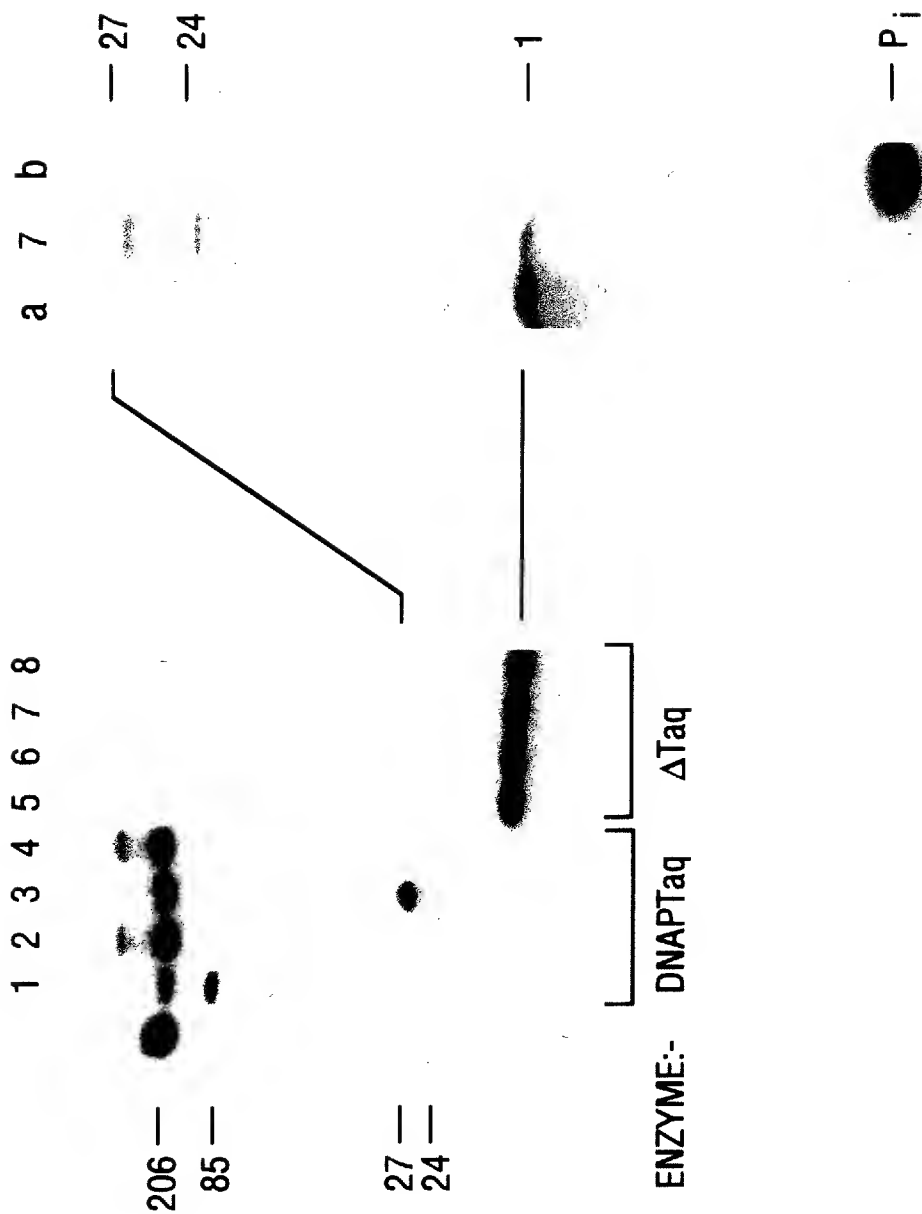


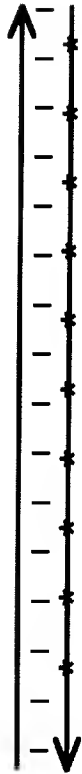
FIG. 25A

FIG. 25B

FIG. 26A



FIG. 26B



\* = 32p



— 206

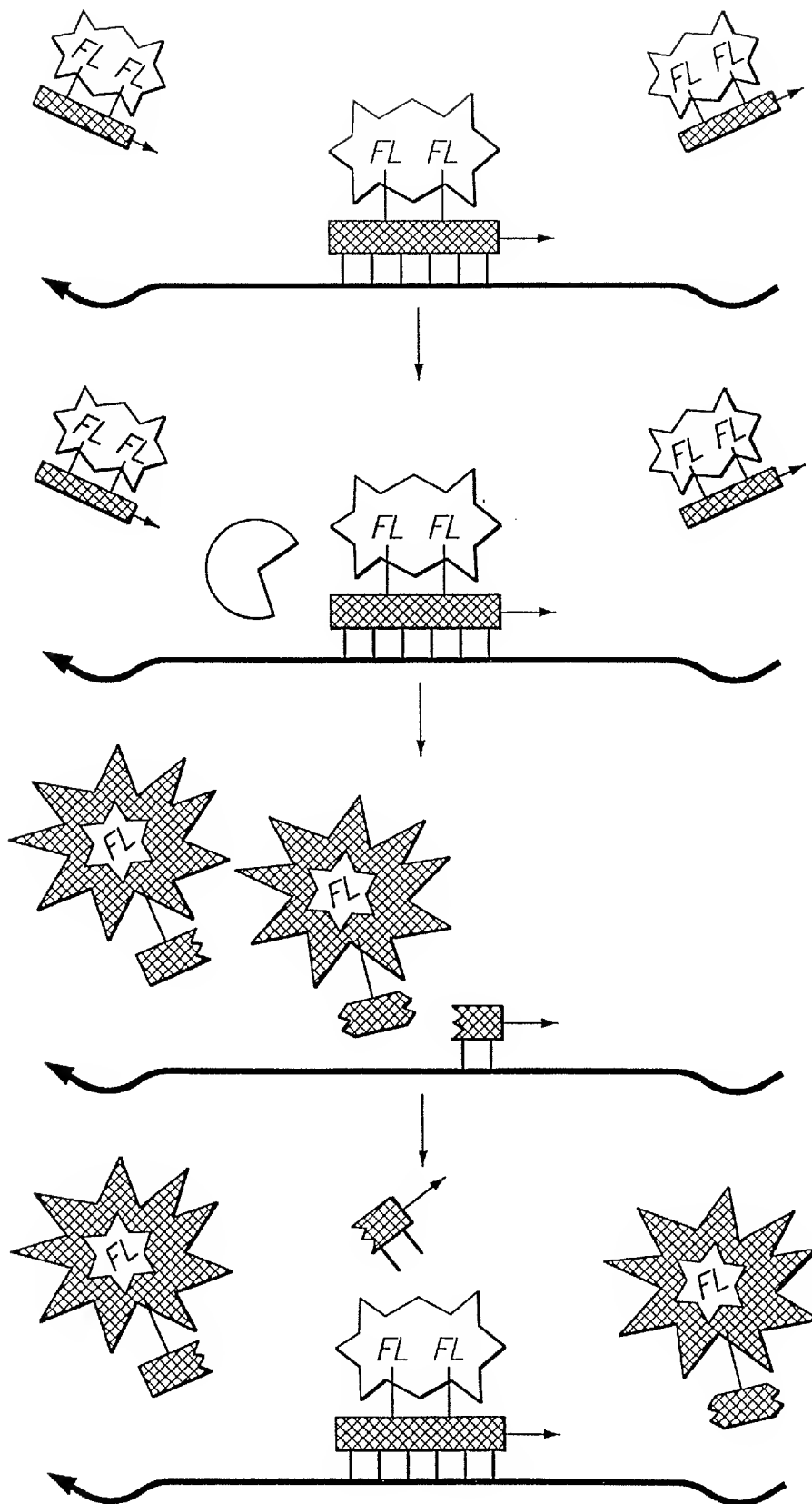


FIGURE 27



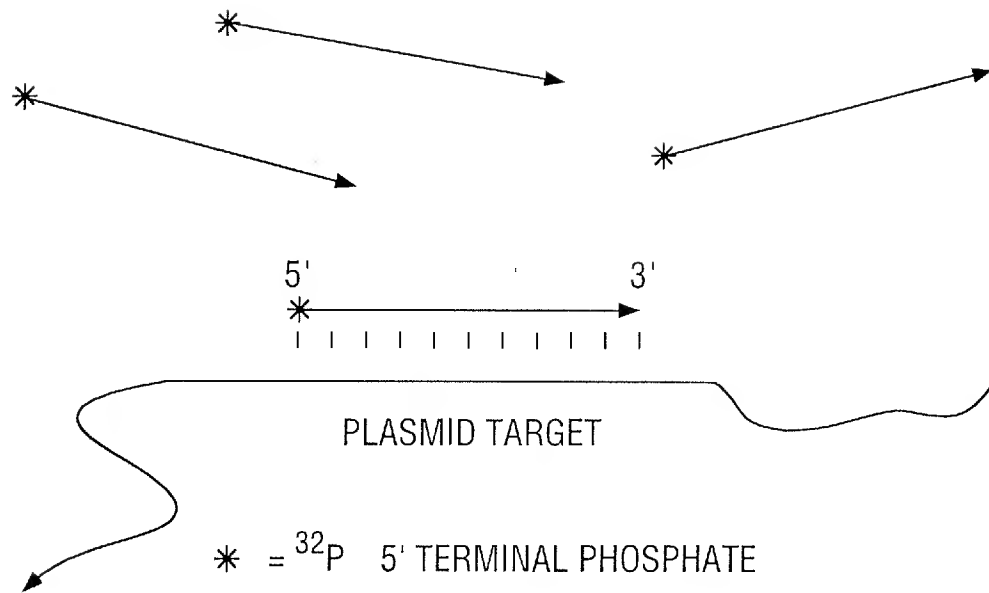
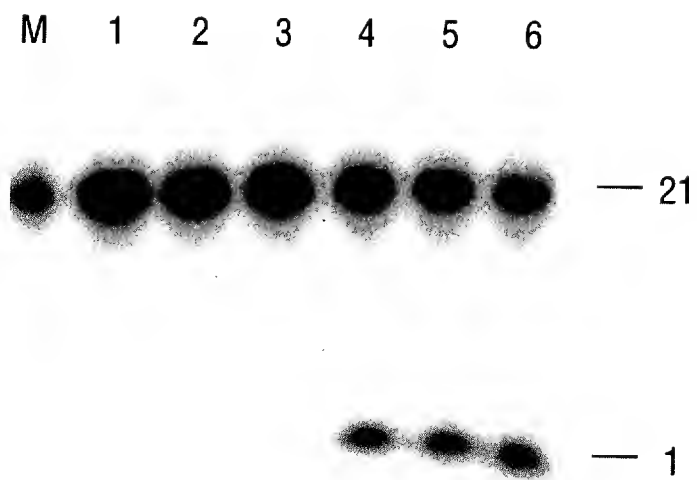


FIGURE 28 A



**FIG. 28B**

FIGURE 29

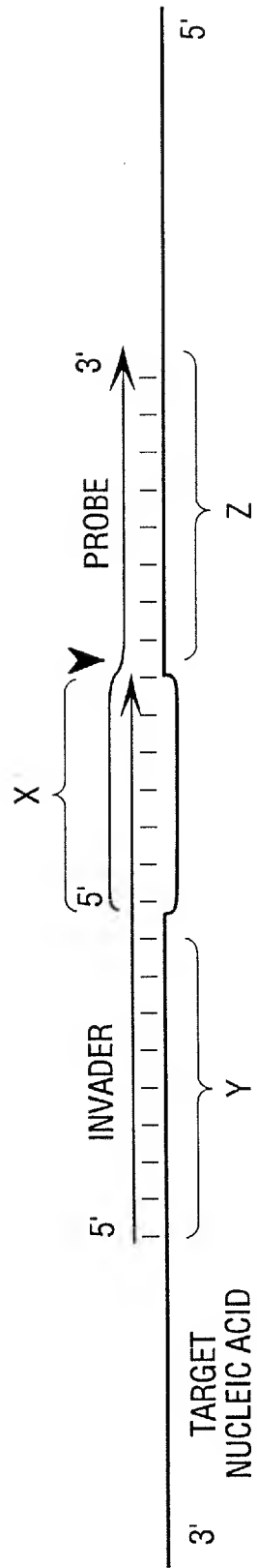


FIGURE 30

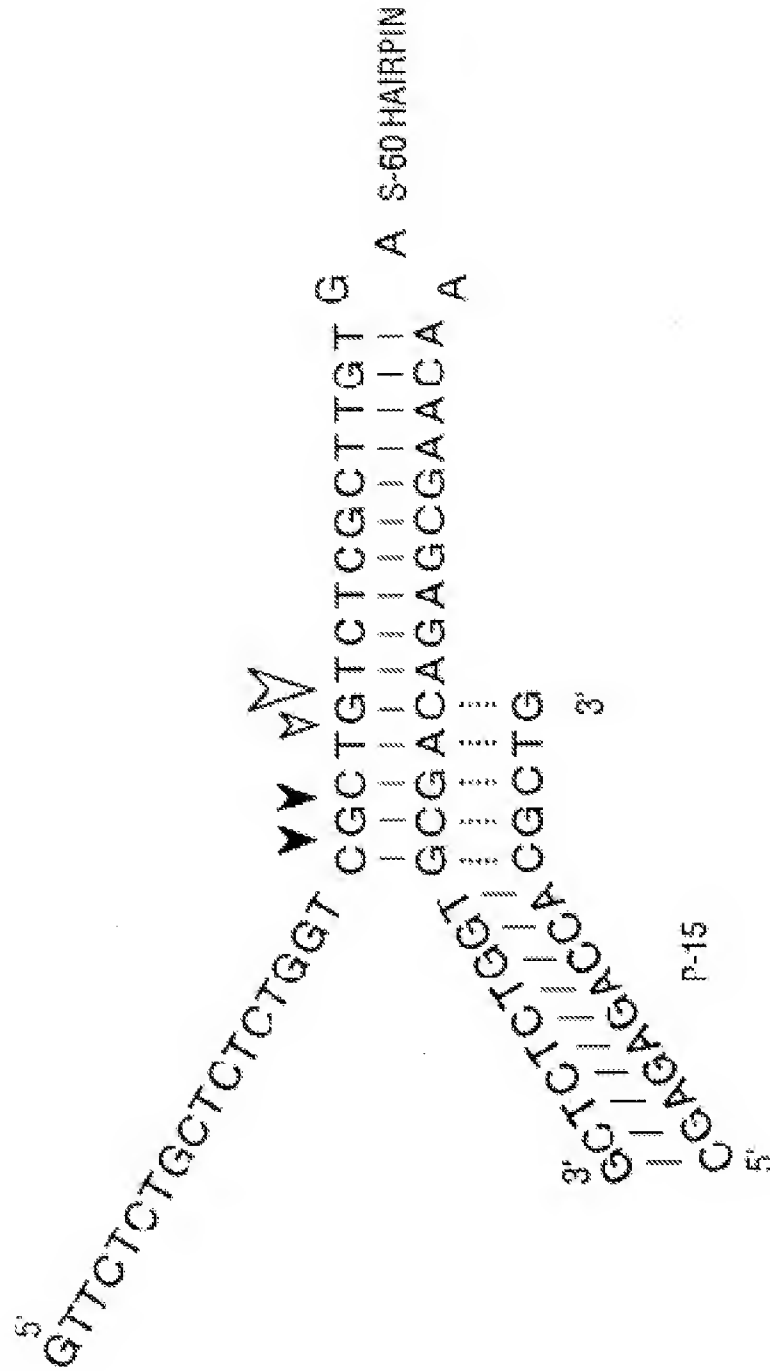


FIGURE 31

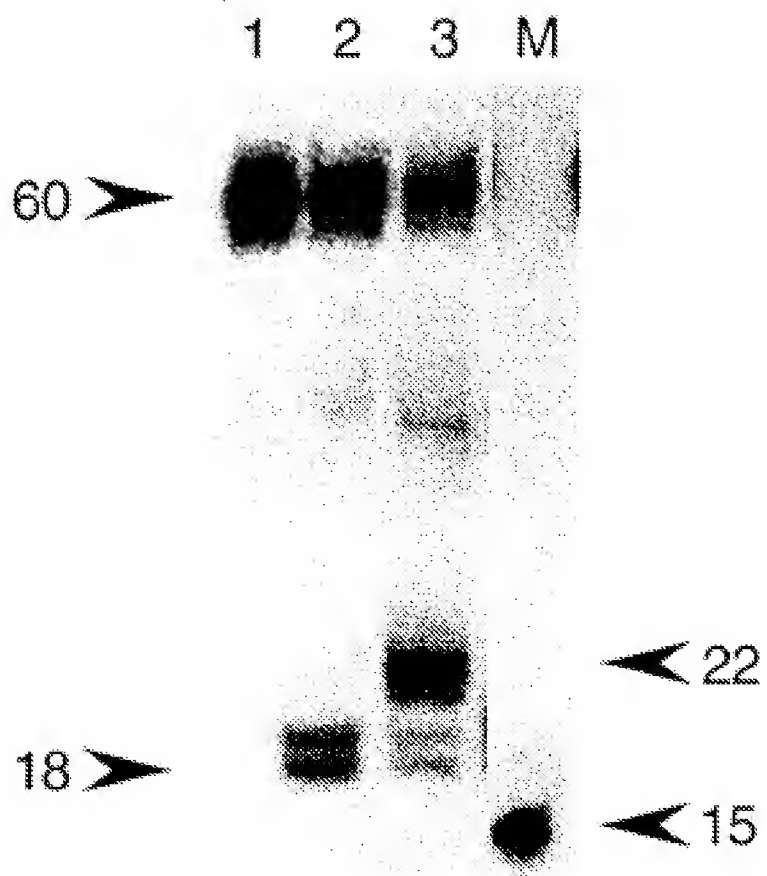


FIGURE 32

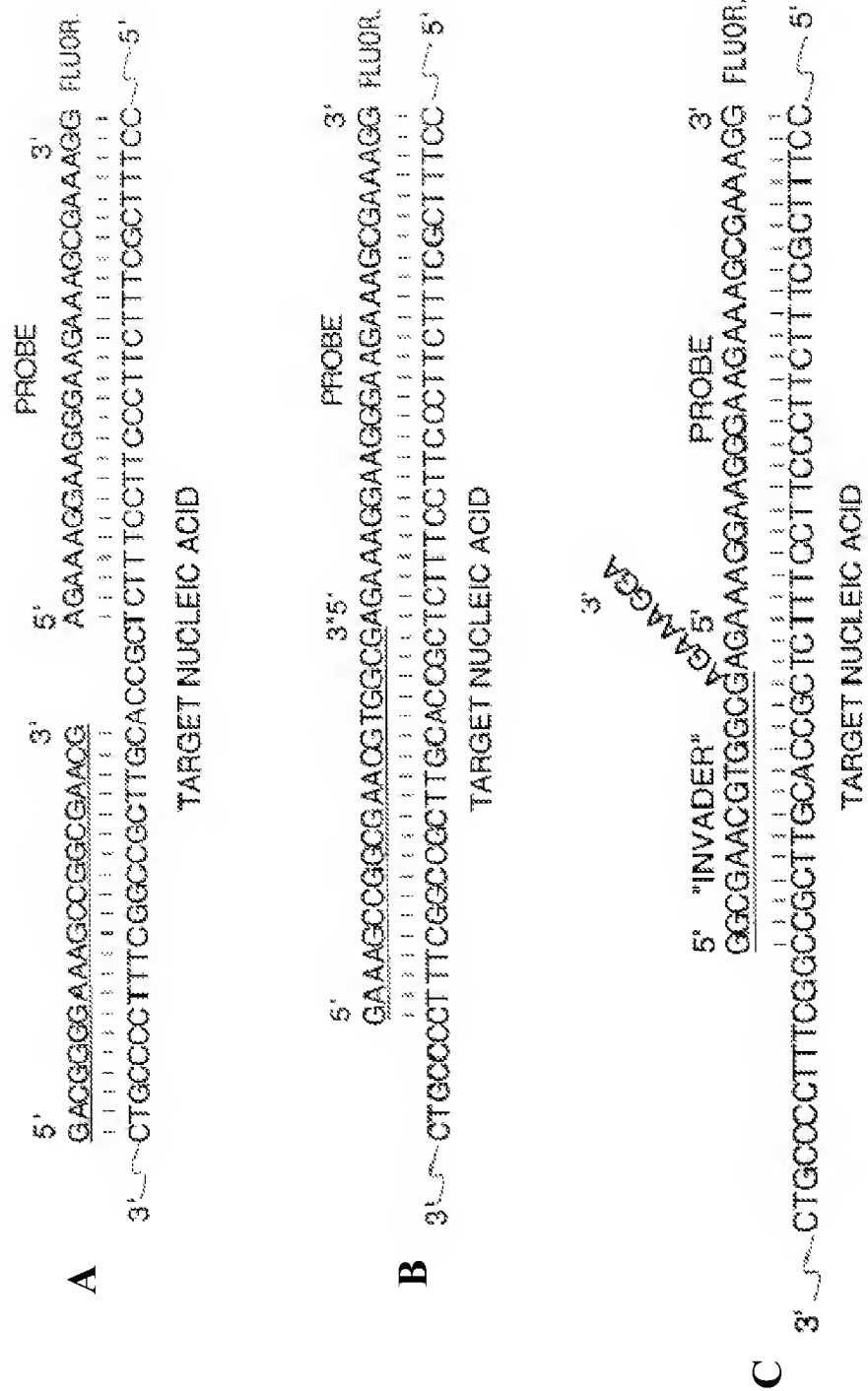


FIGURE 33

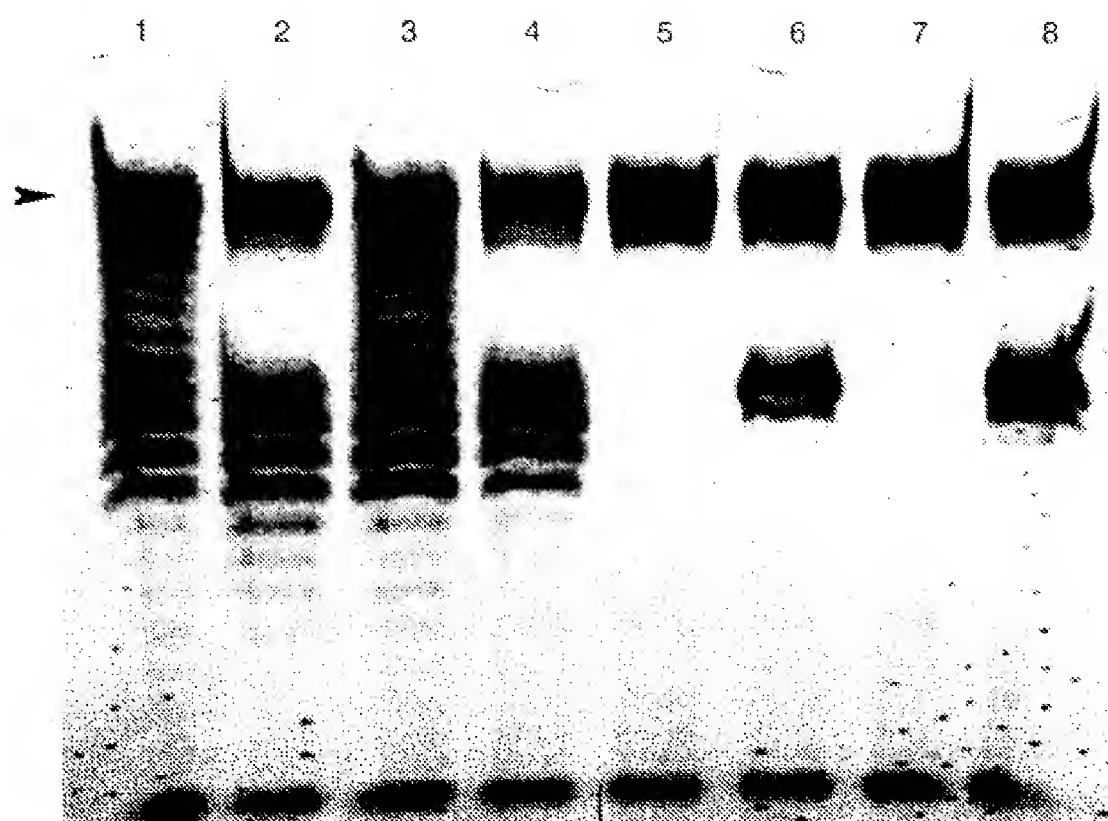


FIGURE 34

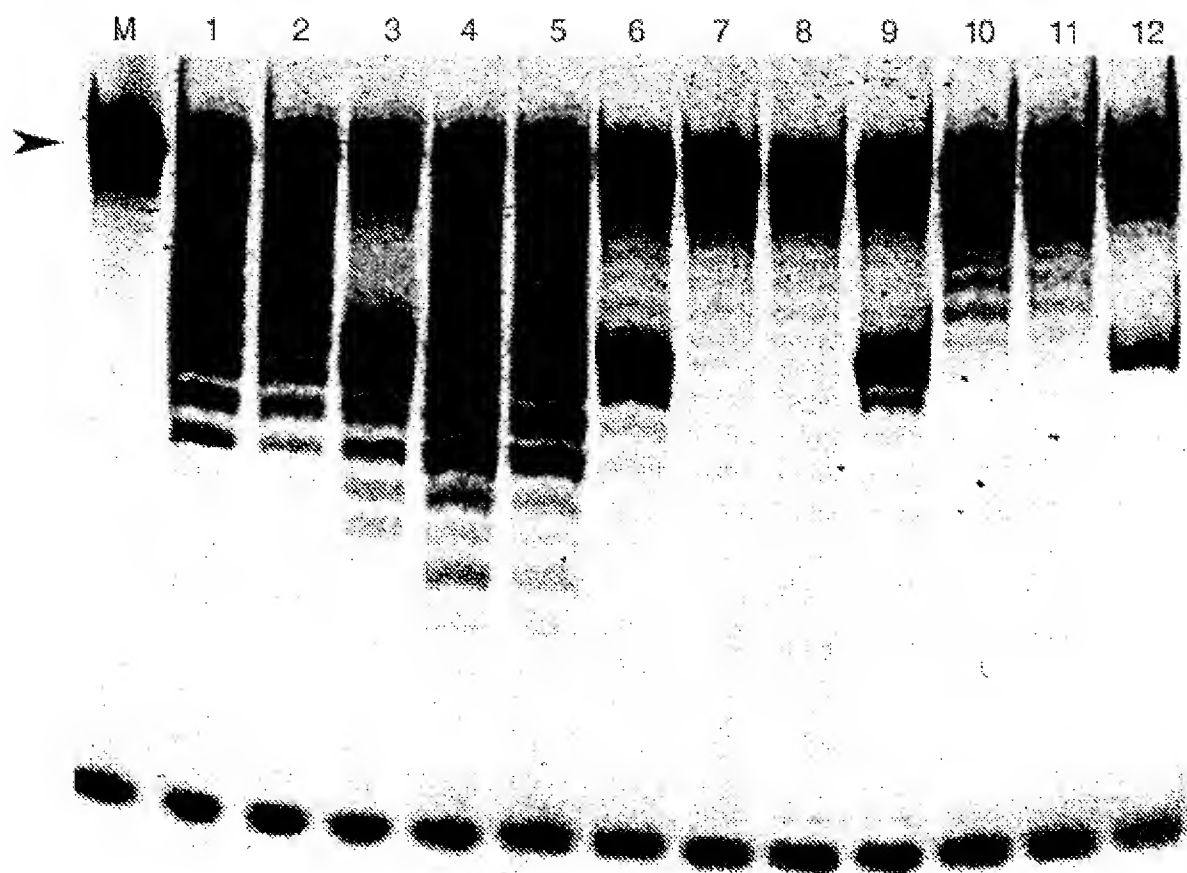




FIGURE 35

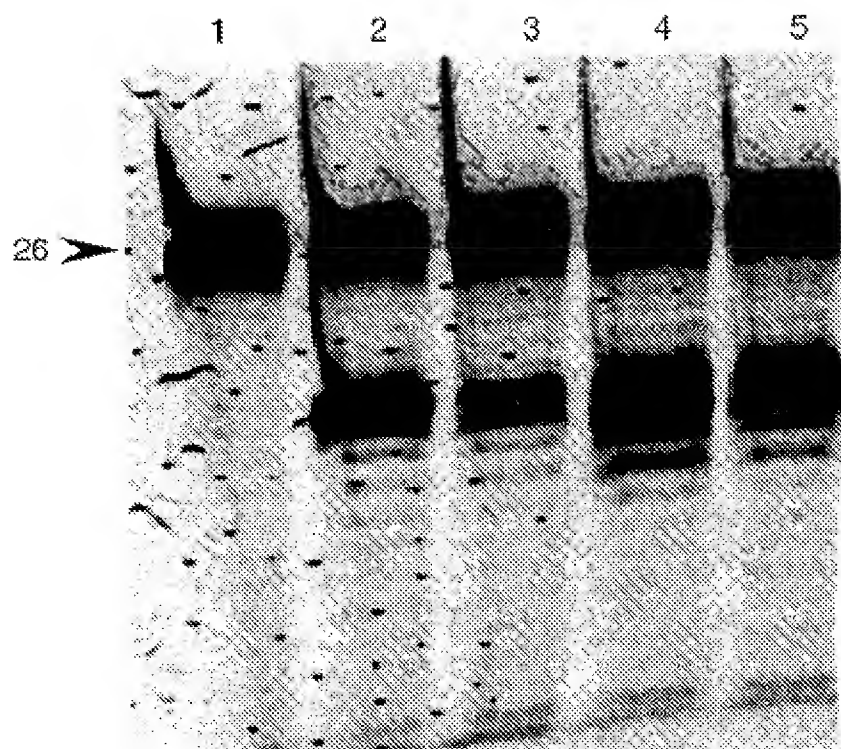


FIGURE 36

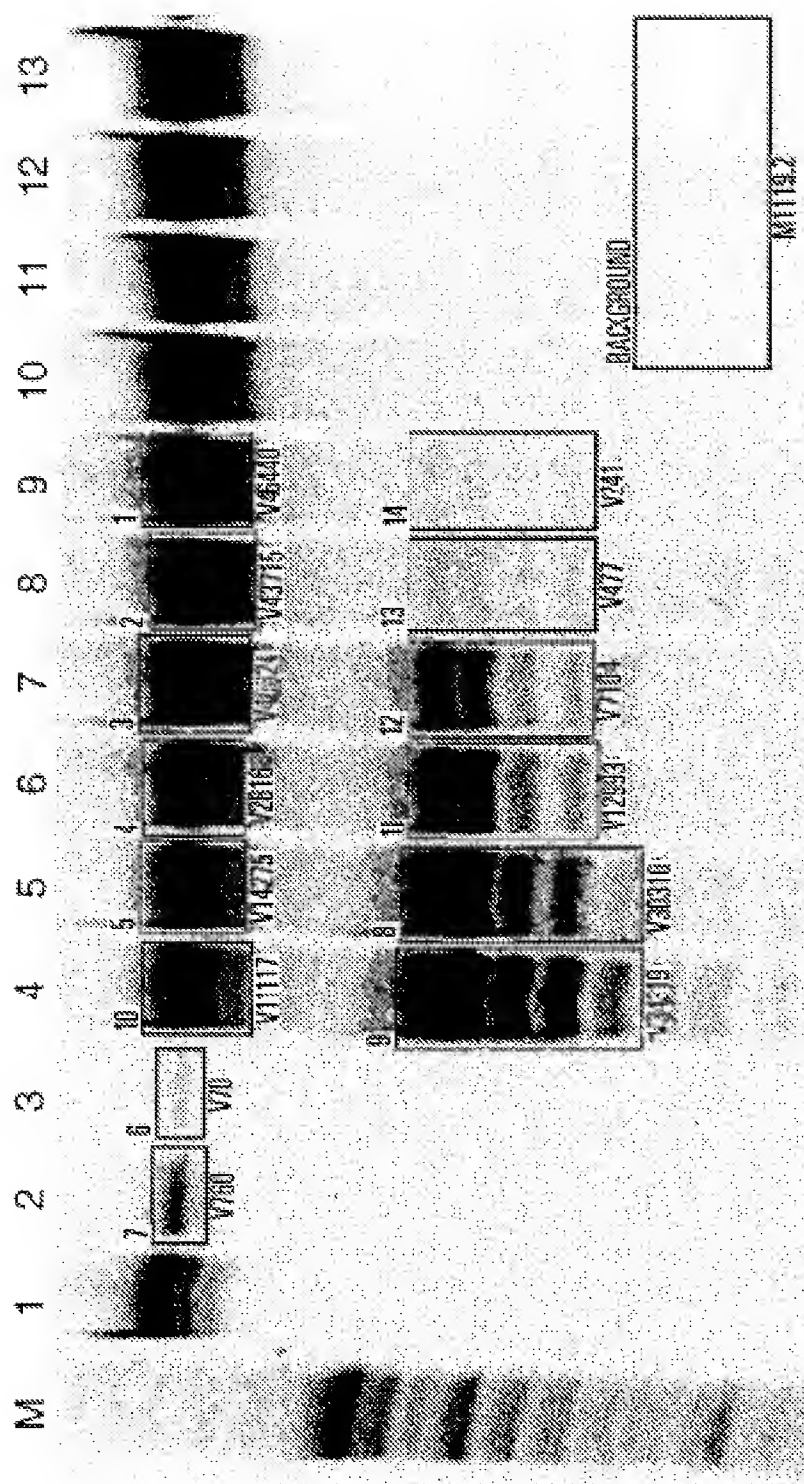


FIGURE 37

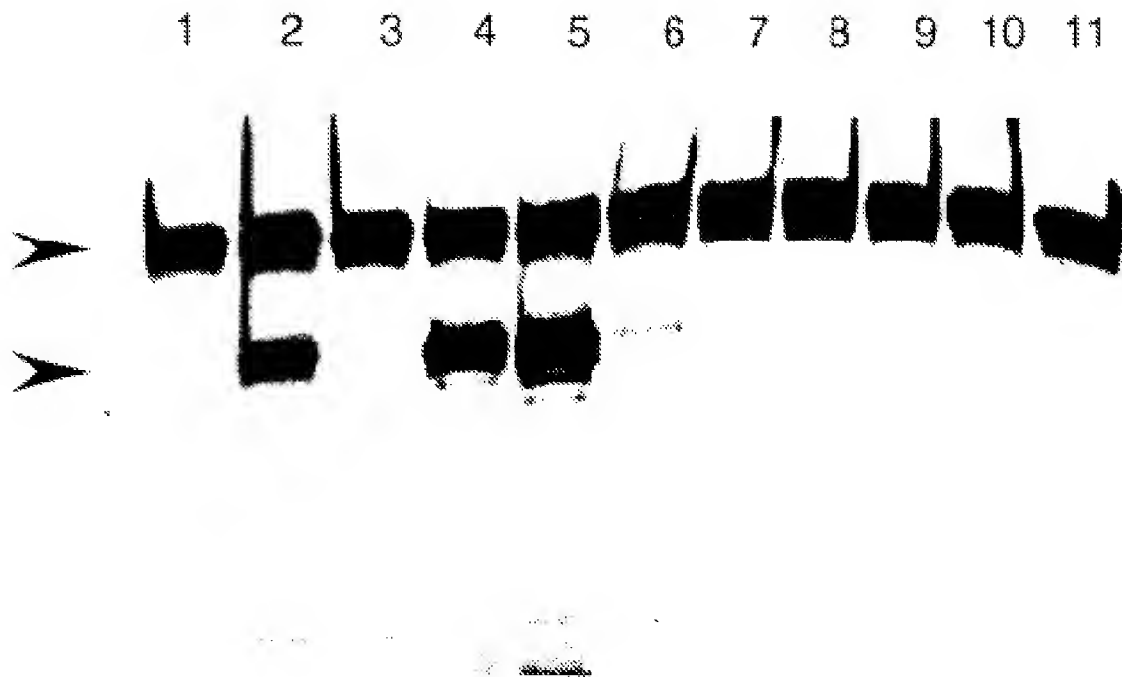


FIGURE 38

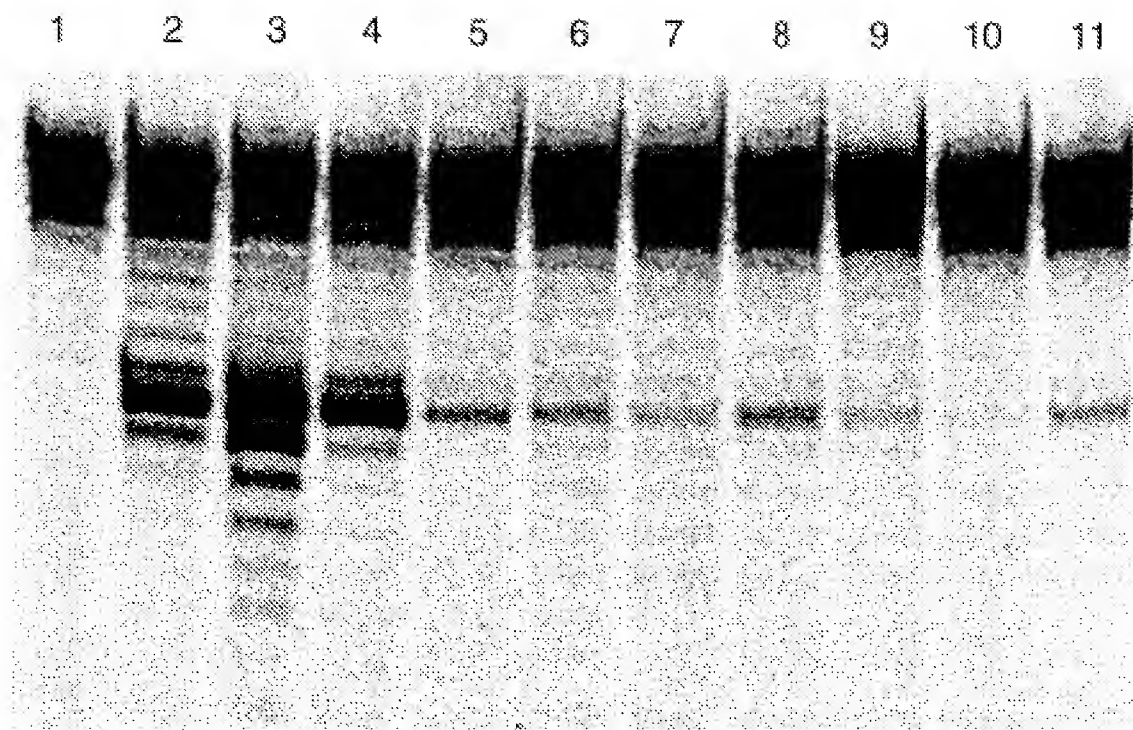


FIGURE 39

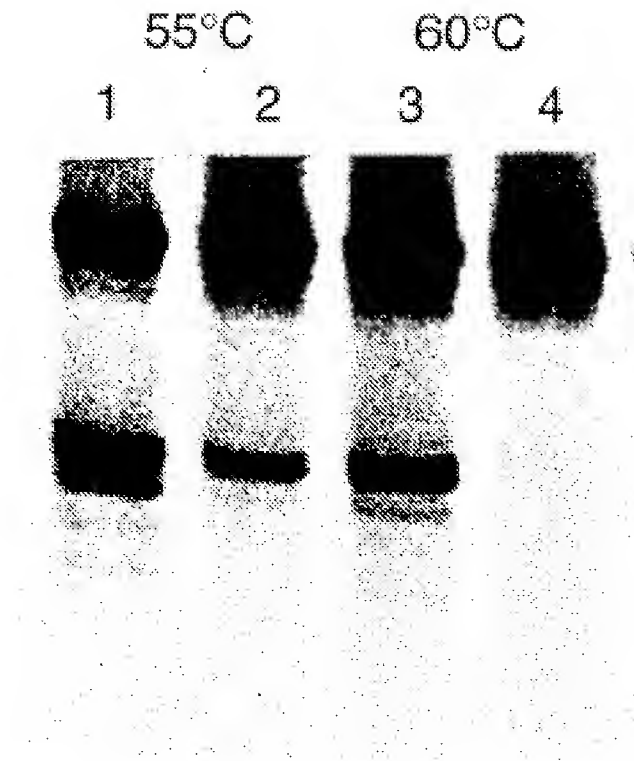


FIGURE 40

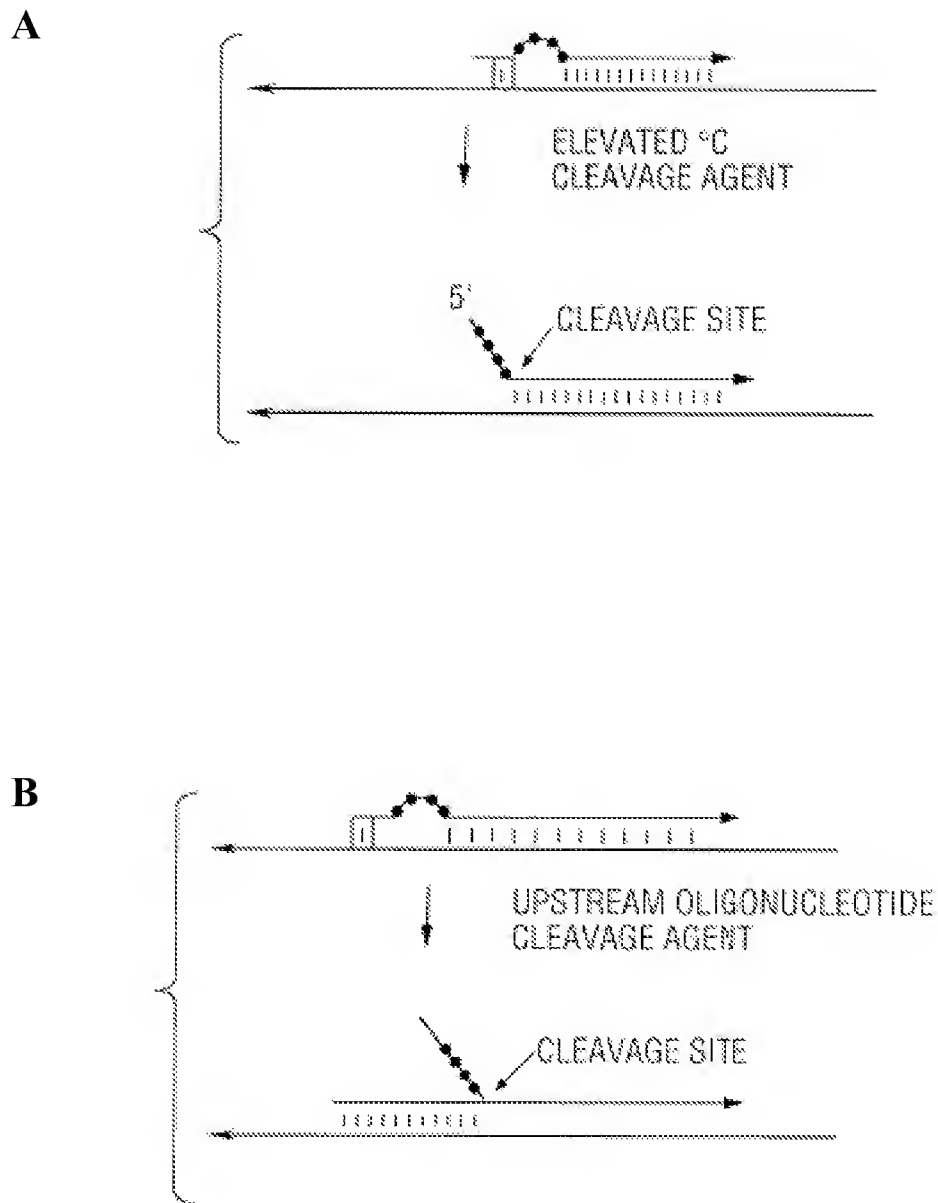


FIGURE 41

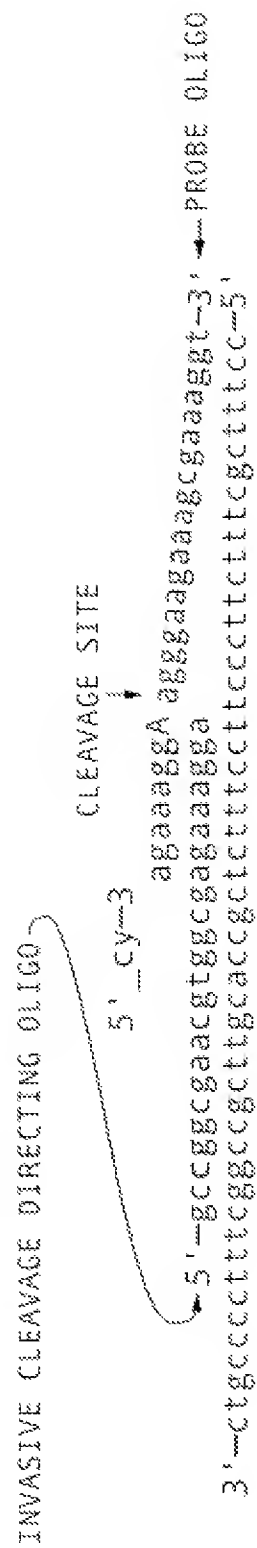
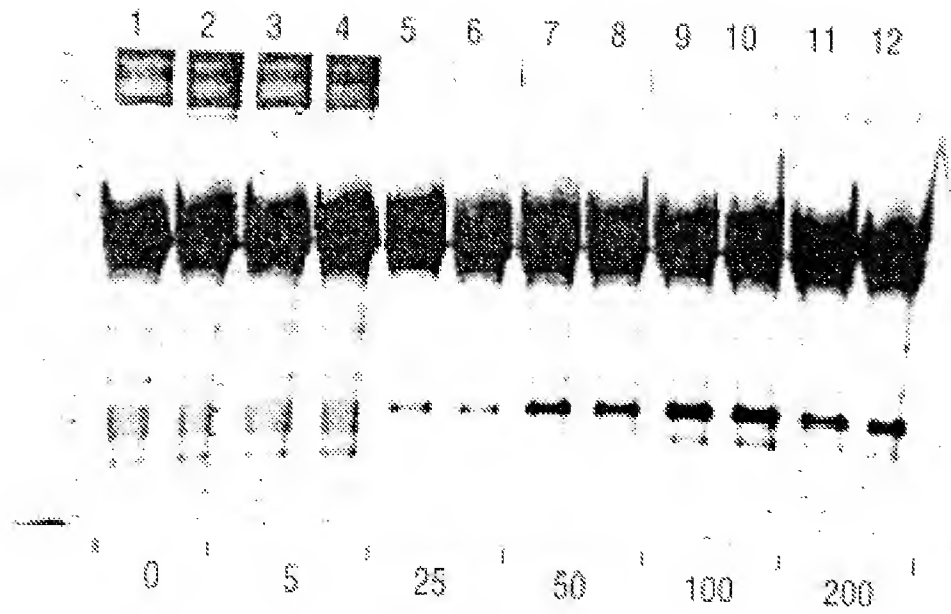
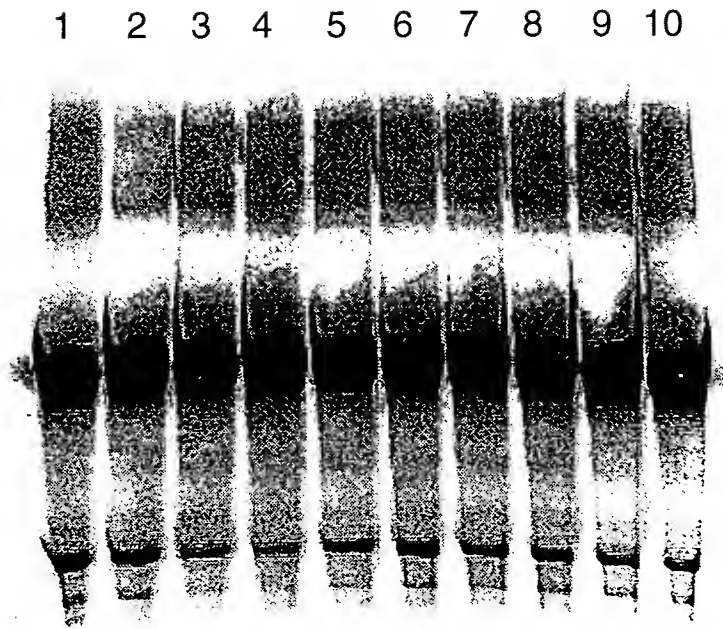


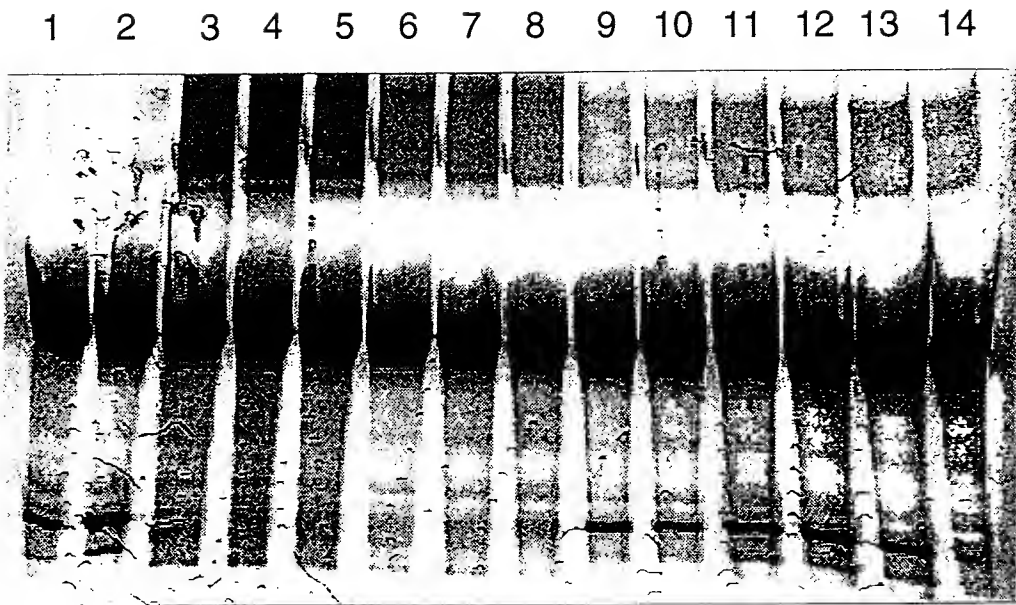
FIGURE 42



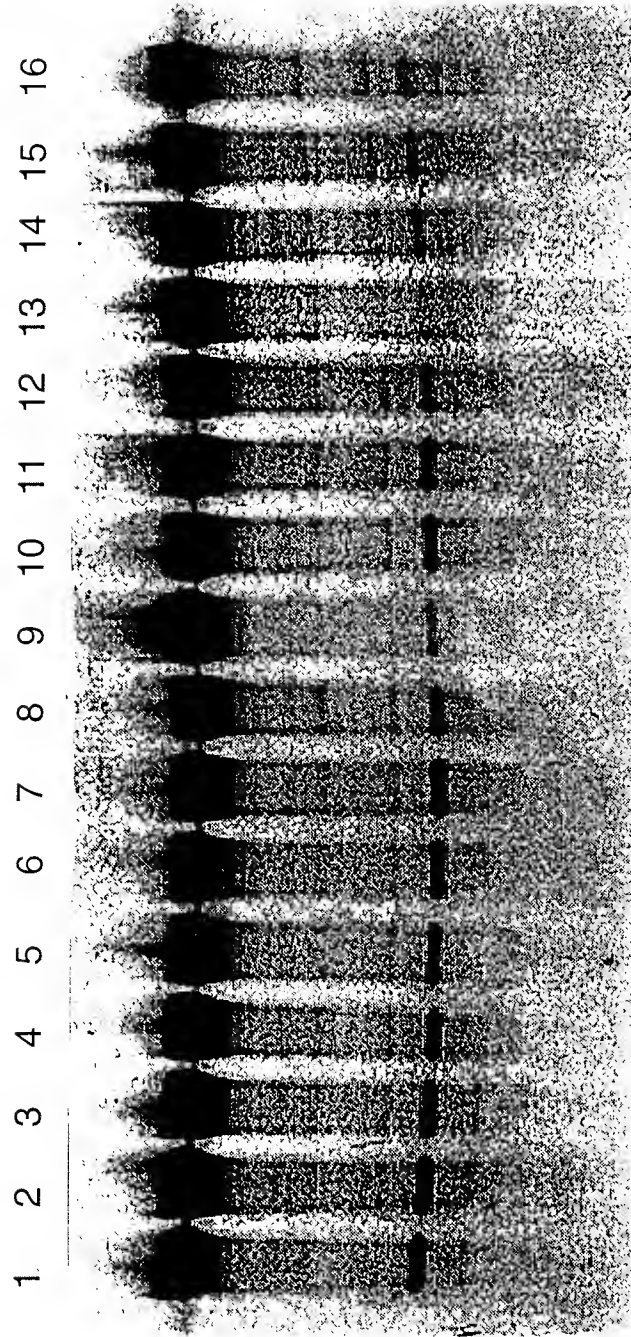




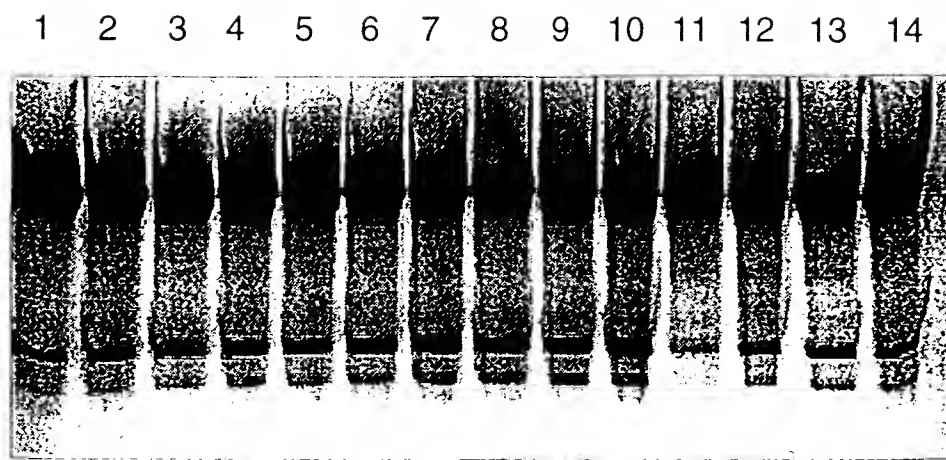
**FIG. 43**



**FIG. 44**



**FIG. 45**



**FIG. 46**

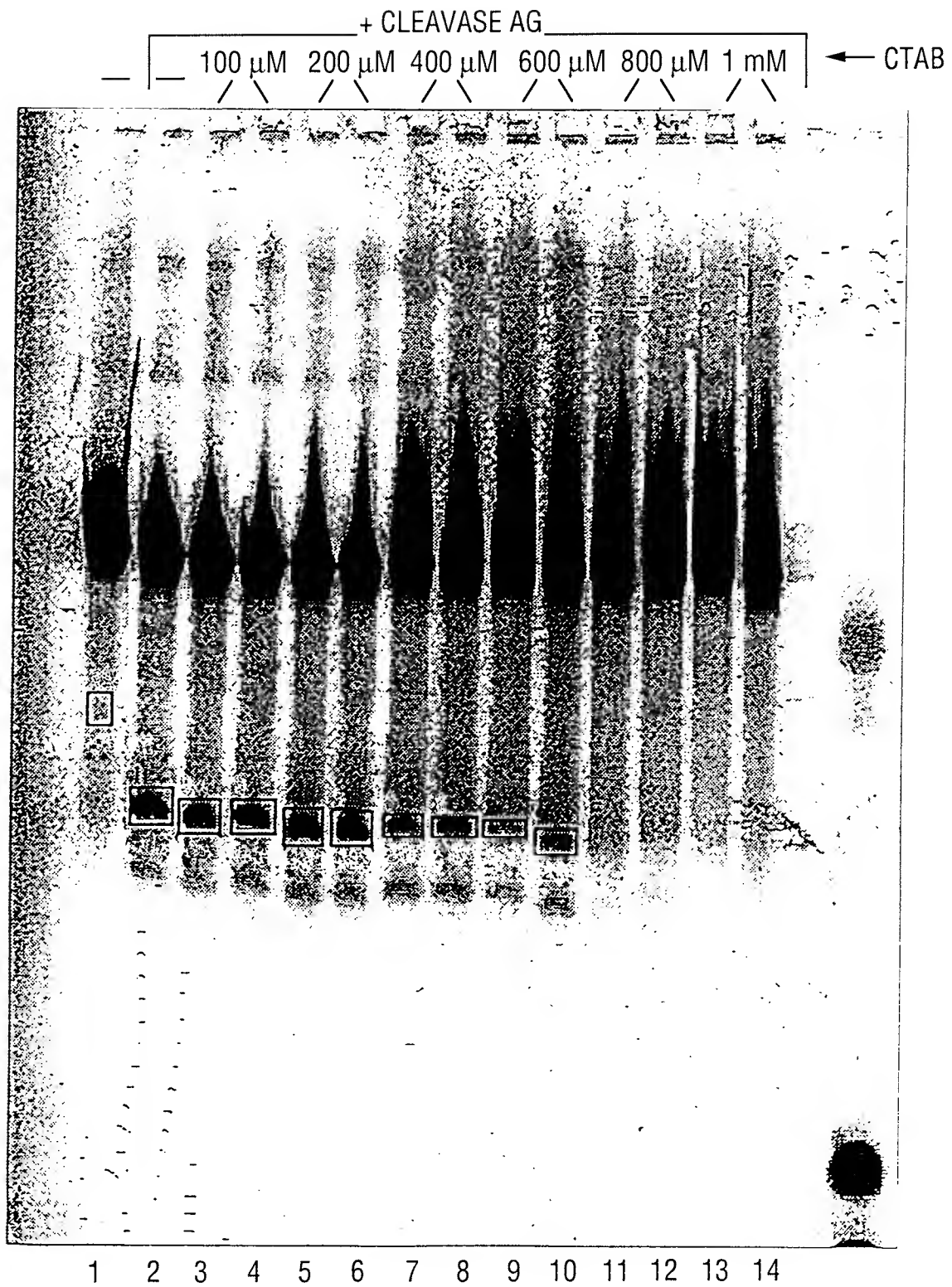
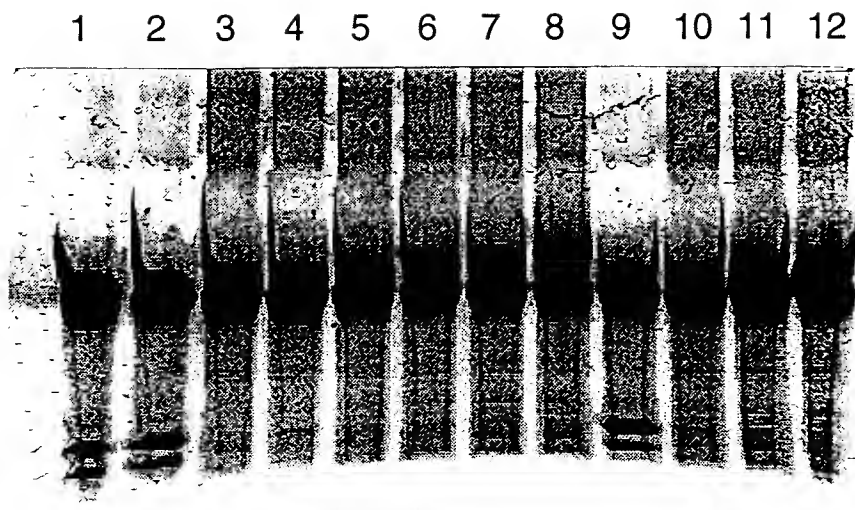
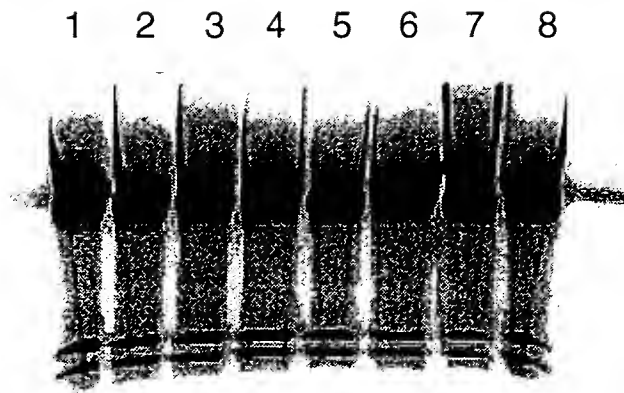


FIG. 47



**FIG. 48**



**FIG. 49**

**FIG. 50**

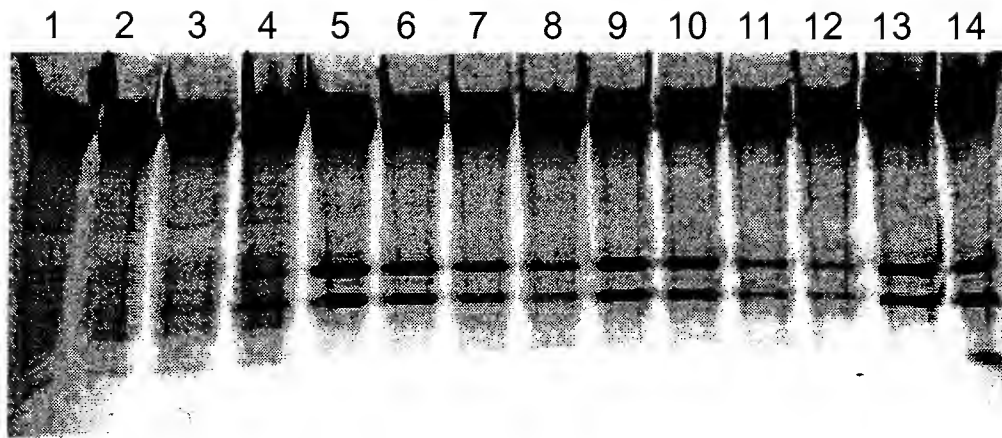




FIGURE 51

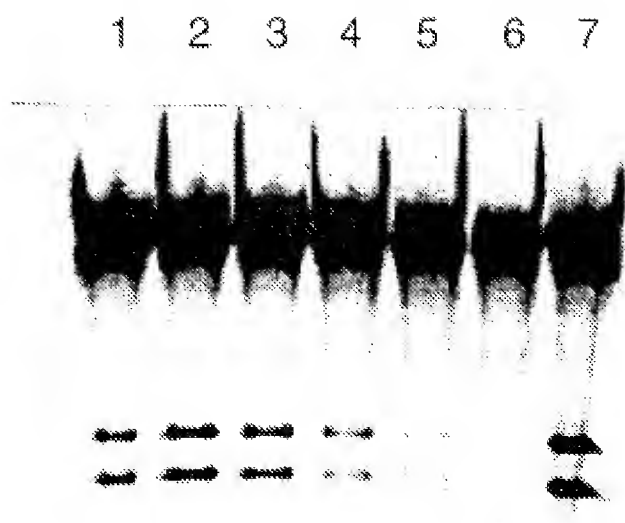


FIGURE 52

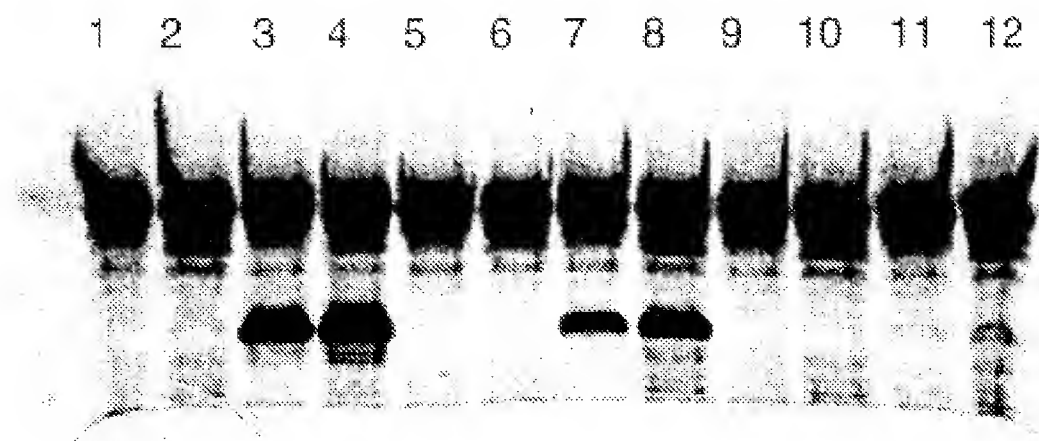
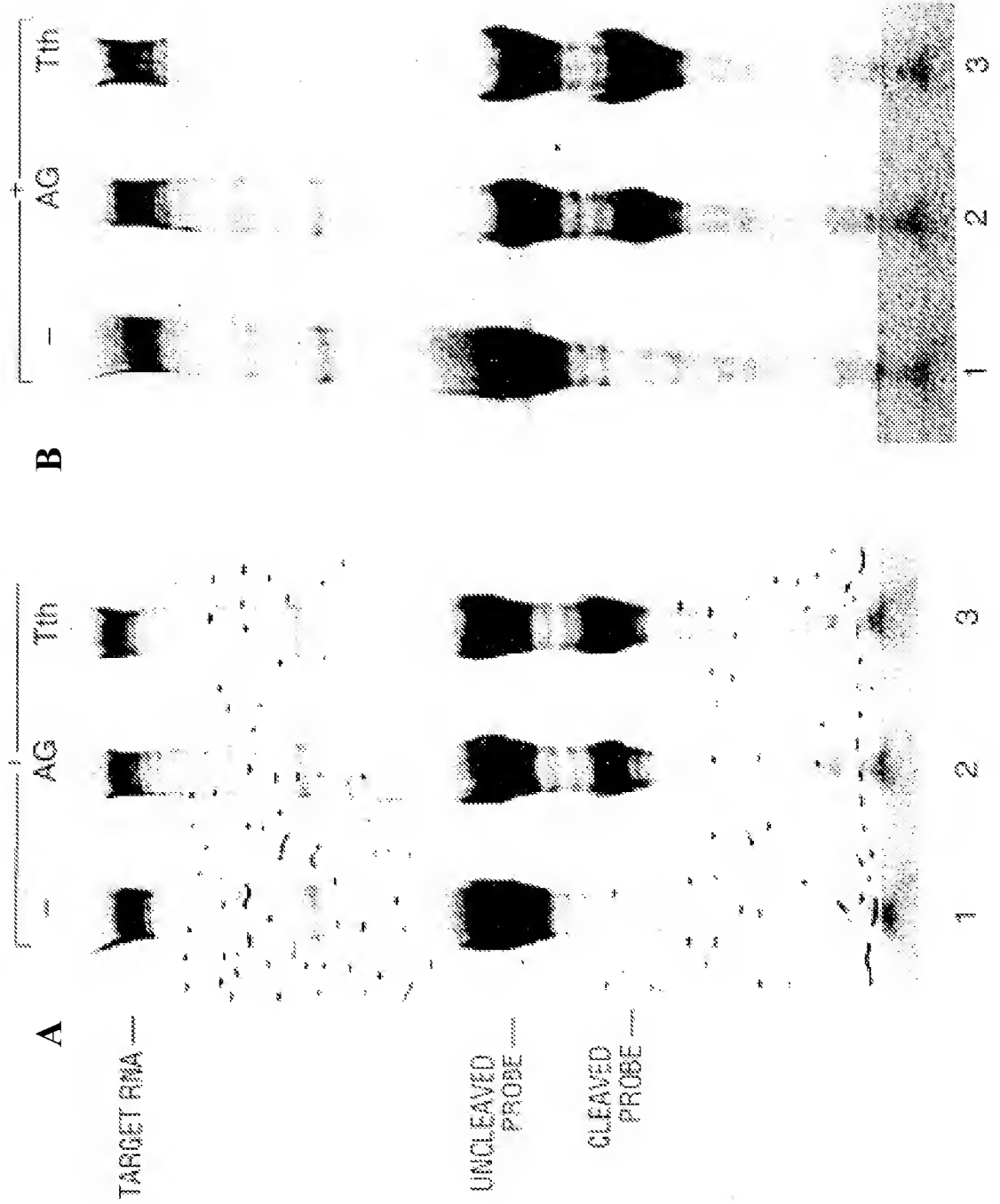
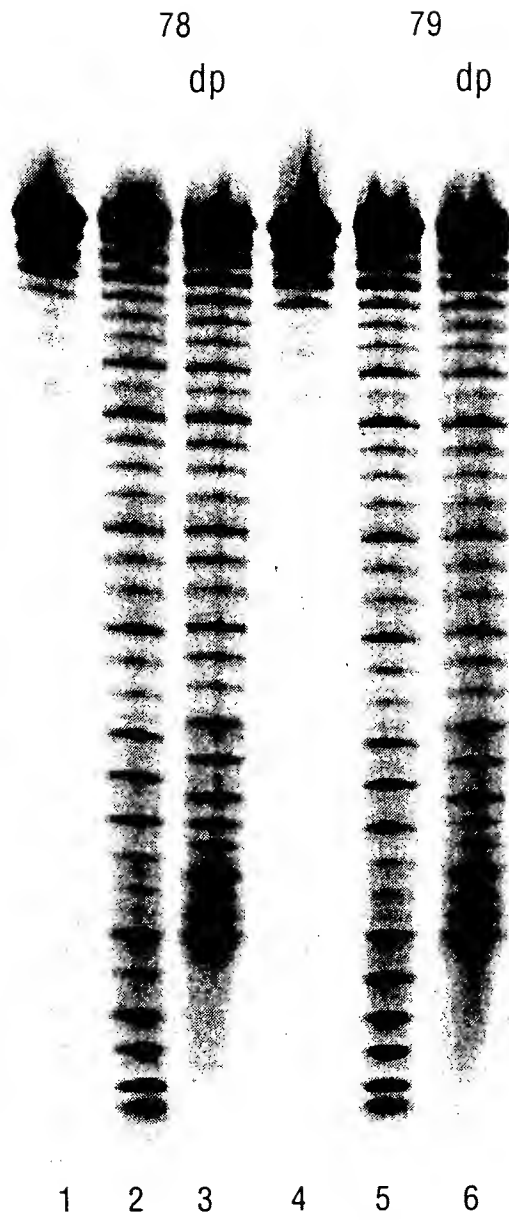


FIGURE 53

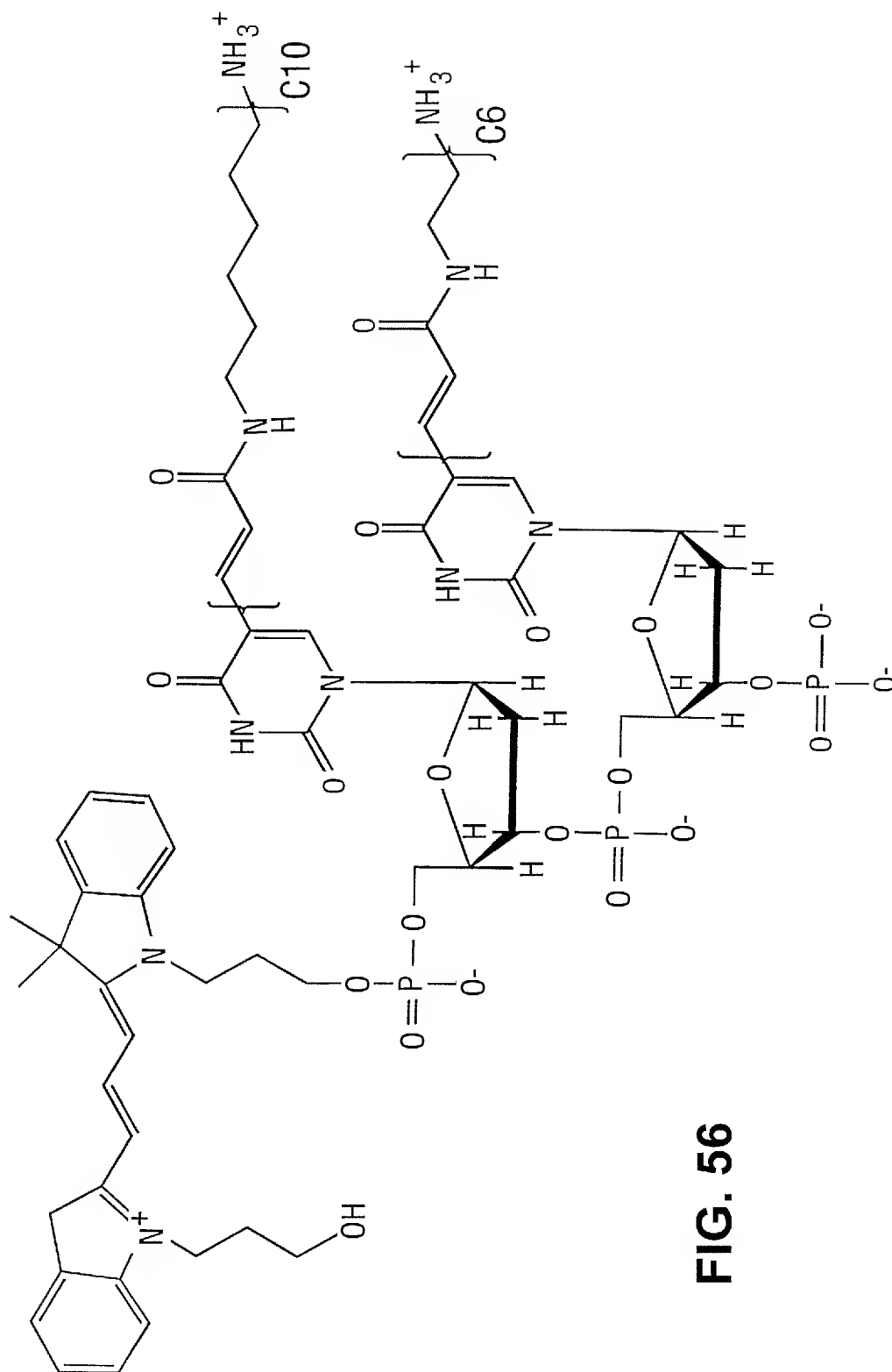






**FIG. 55**

70 (C10 amino T's)  
74 (C6 amino T's)



**FIG. 56**

75

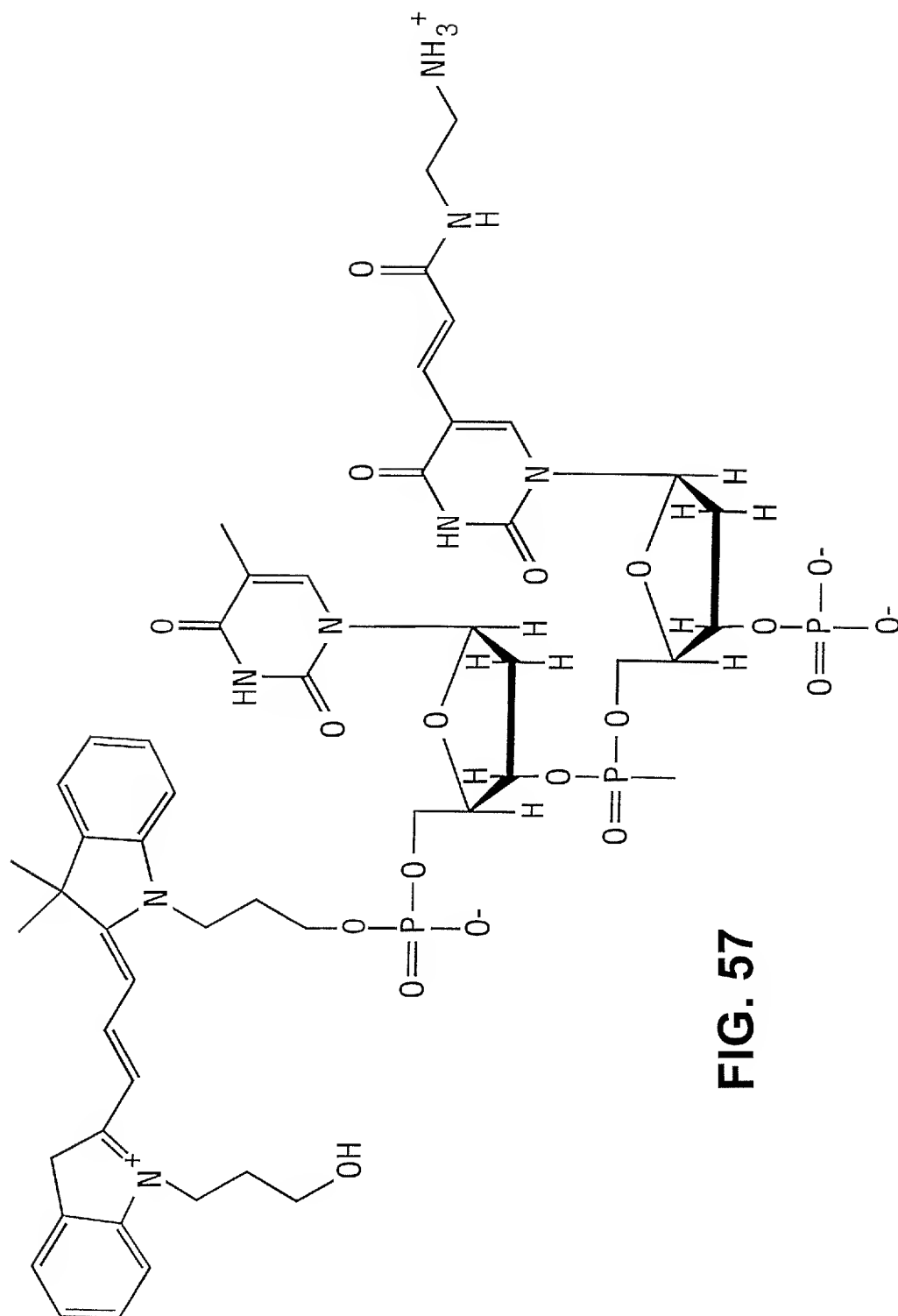
**FIG. 57**

FIGURE 58

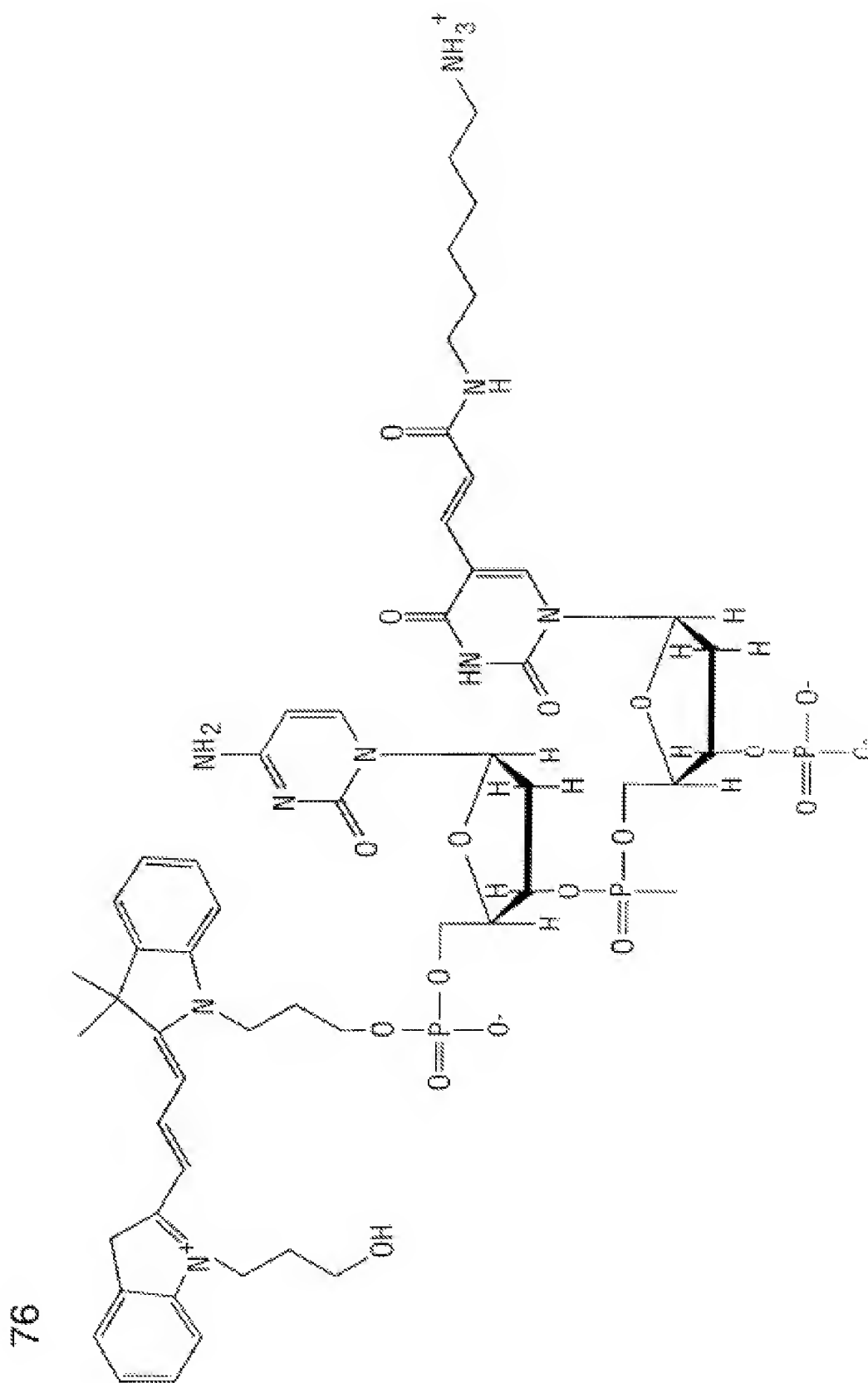




FIGURE 59

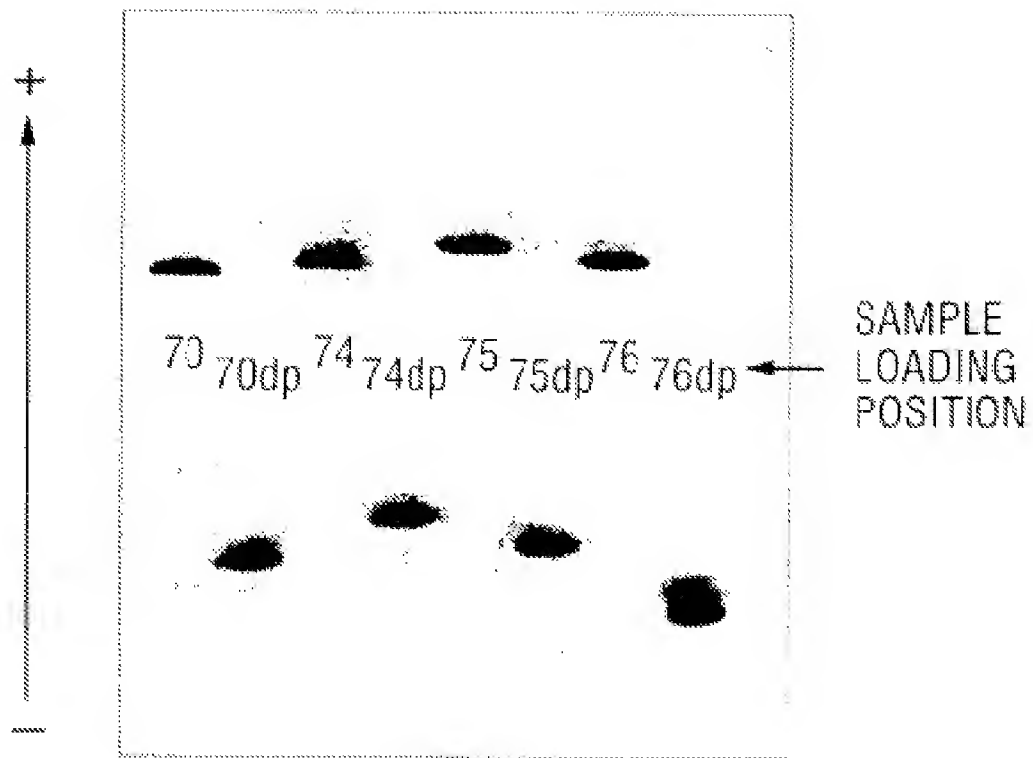


FIGURE 60

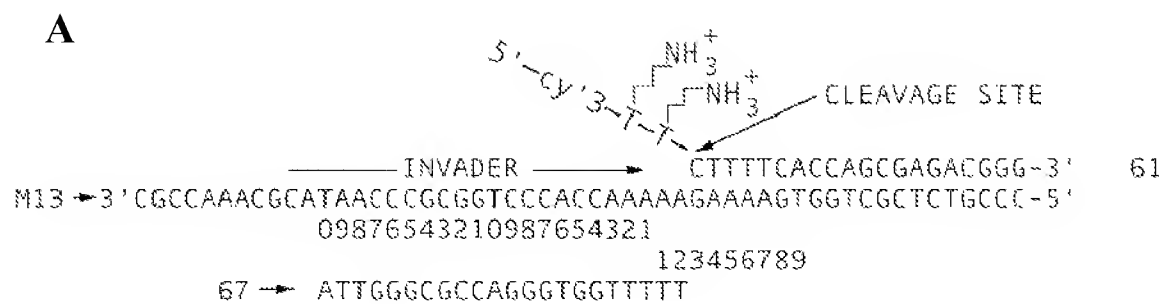
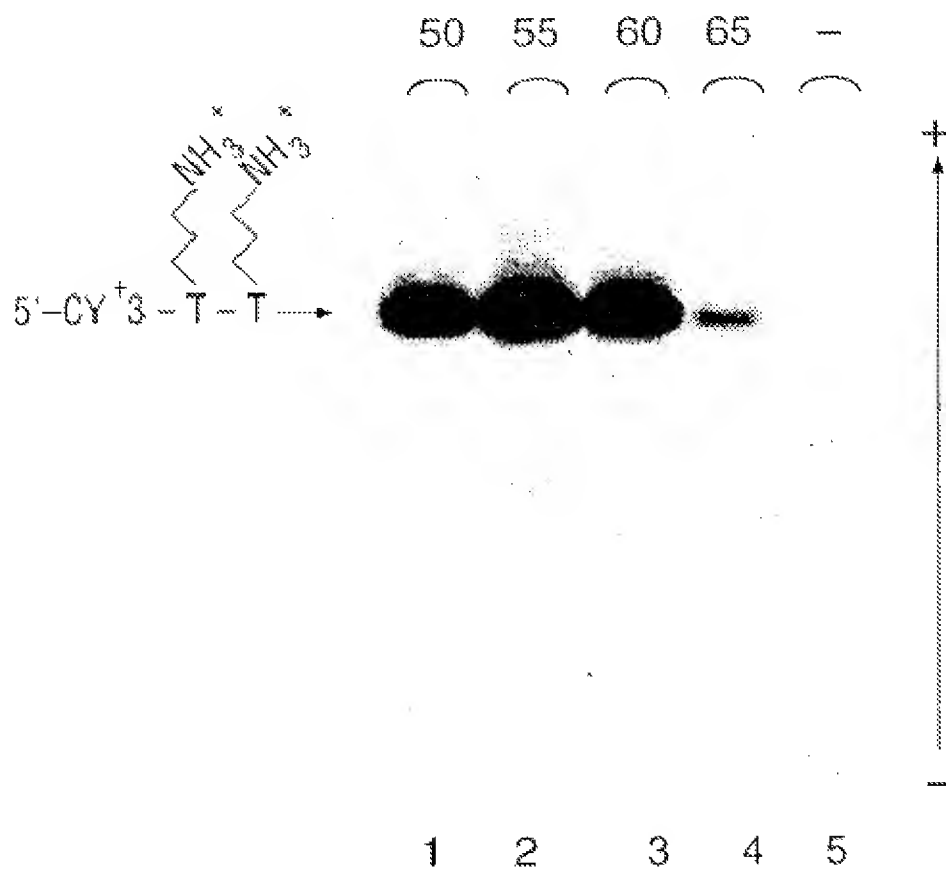
**B**

FIGURE 61

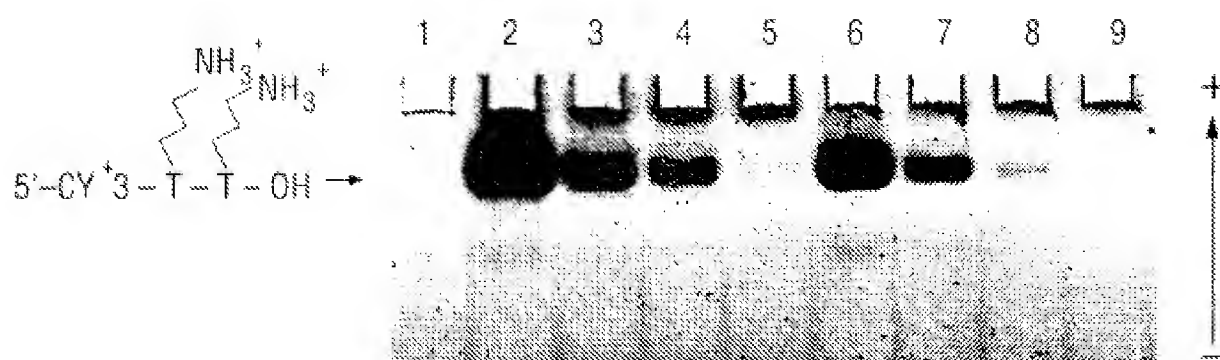


FIGURE 62

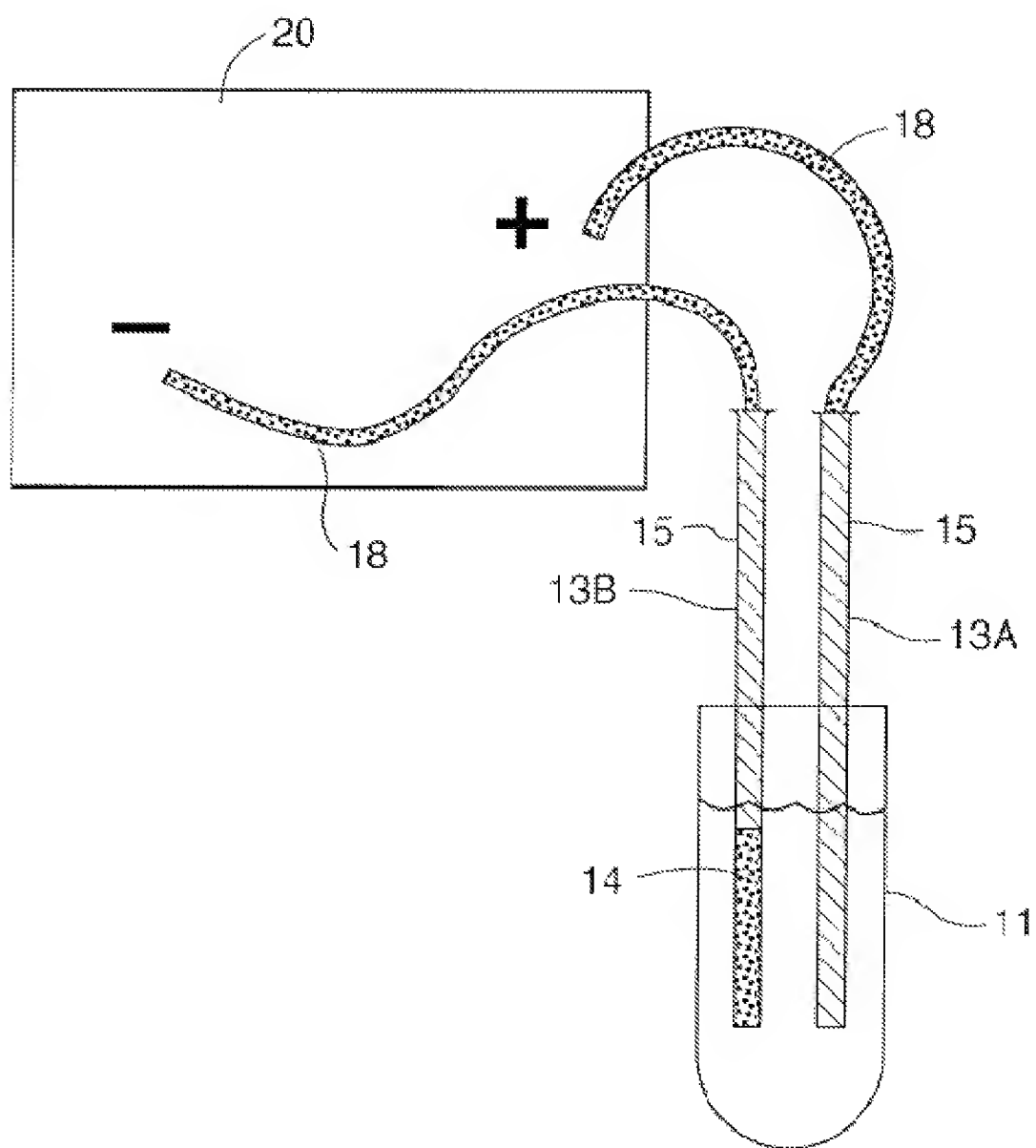


FIGURE 63

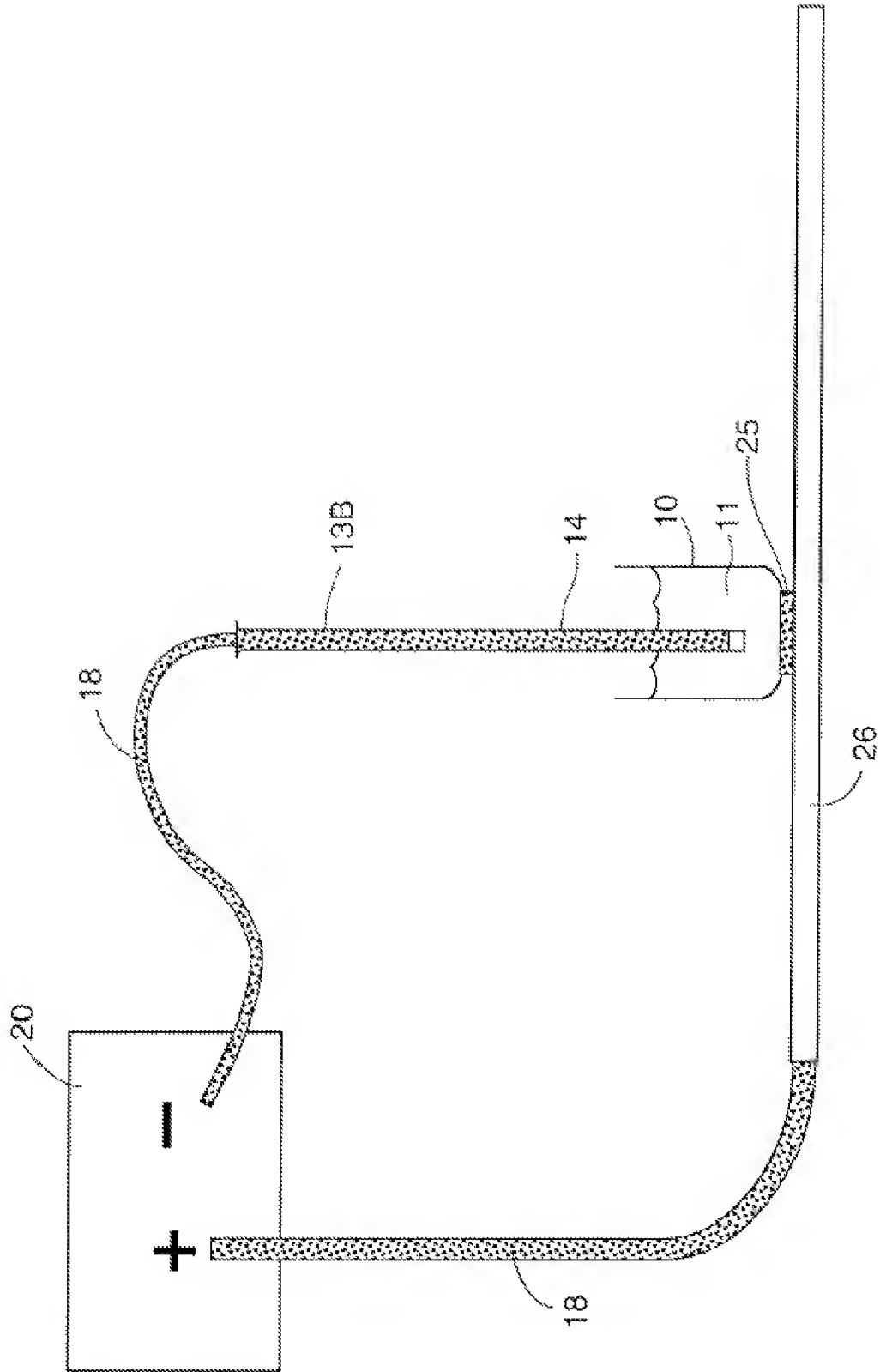


FIGURE 64

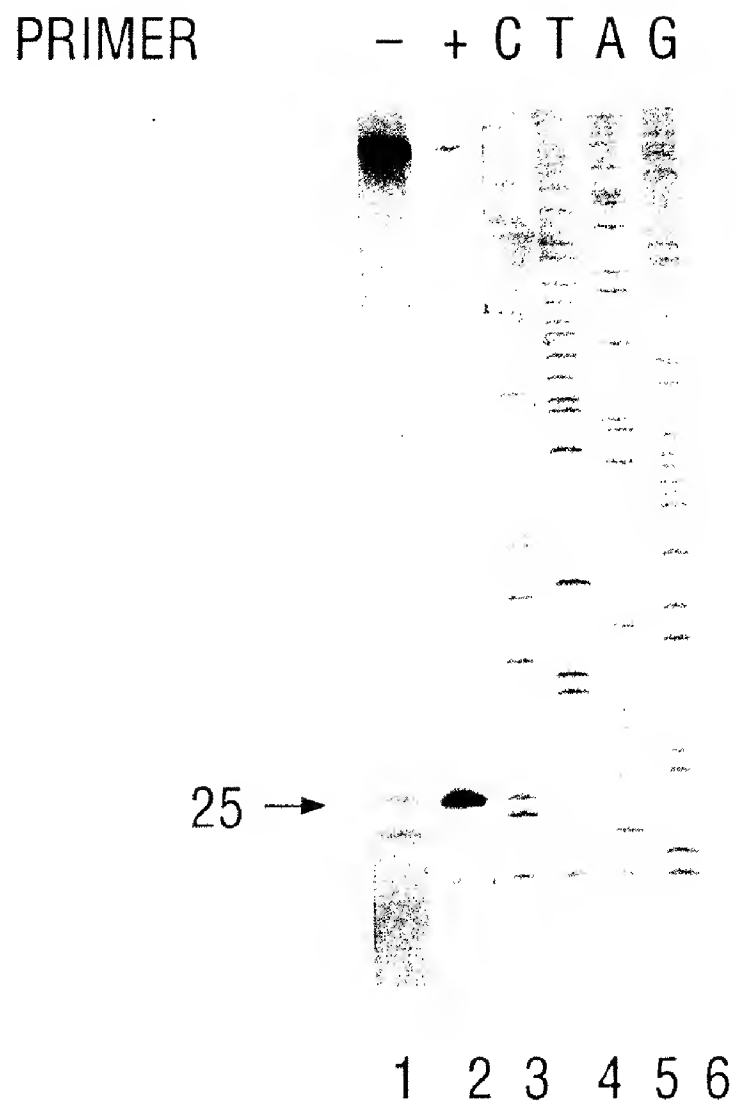


FIGURE 65

**A****B****C****D**

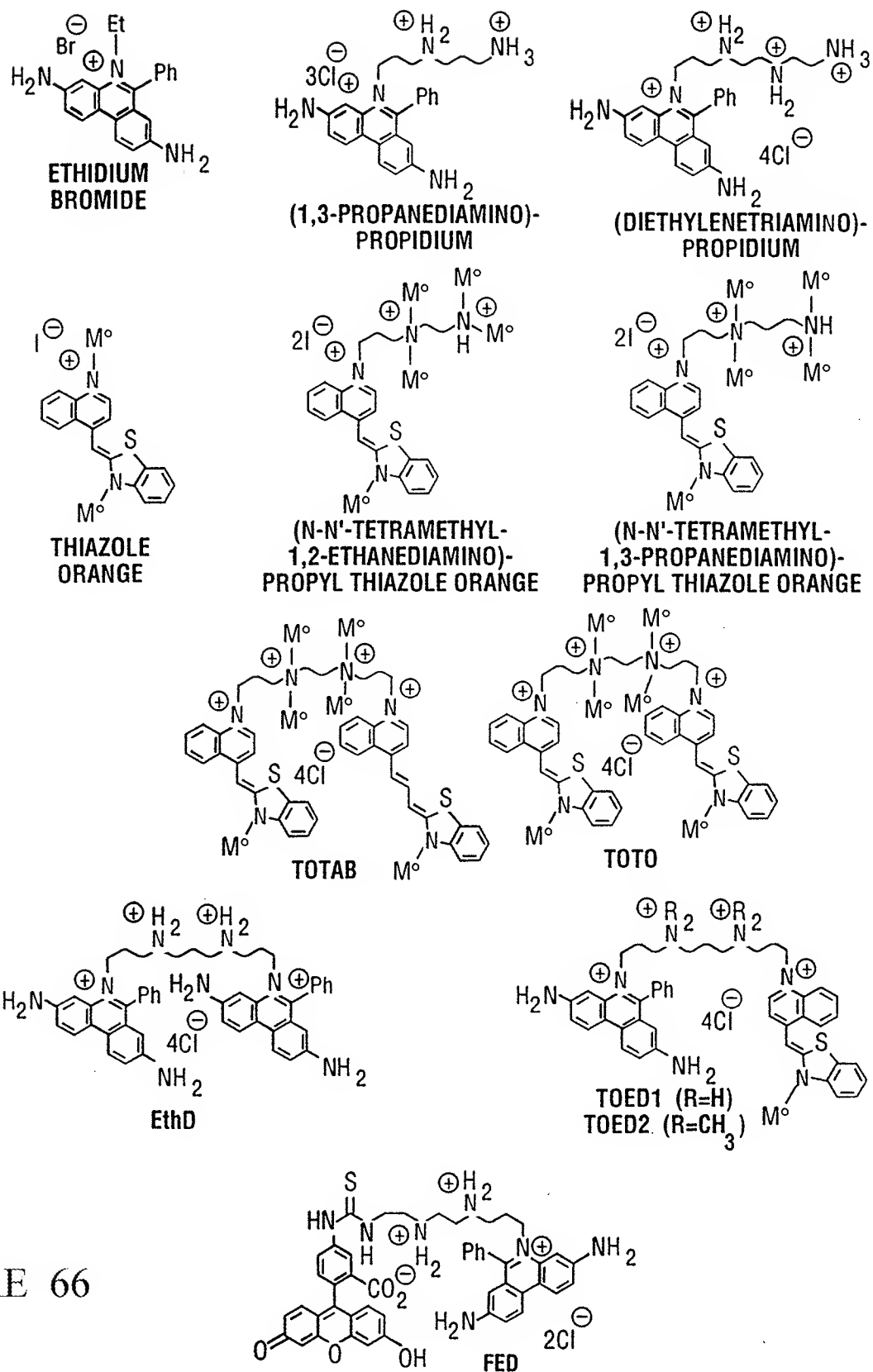


FIGURE 66



FIGURE 67

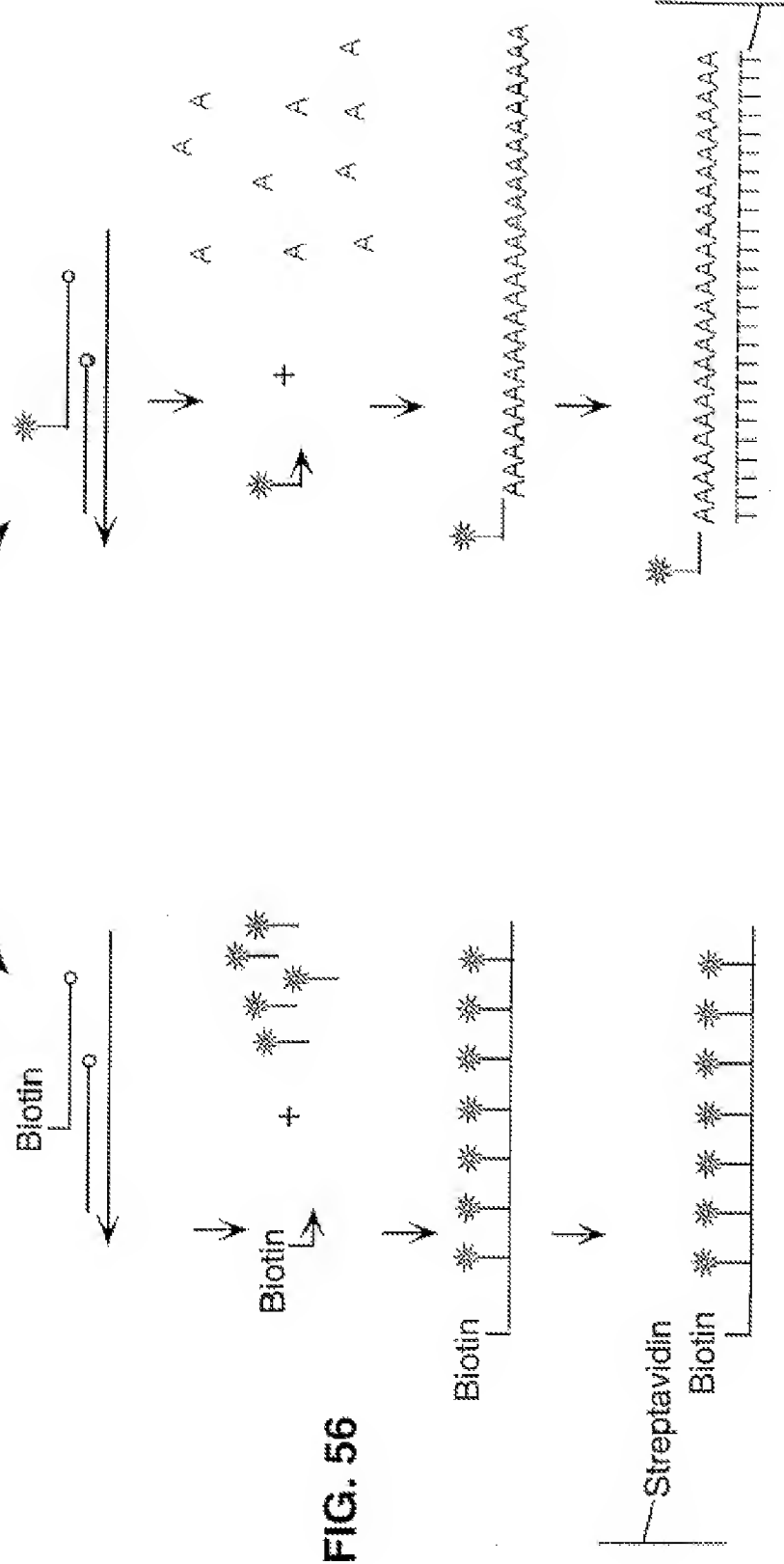
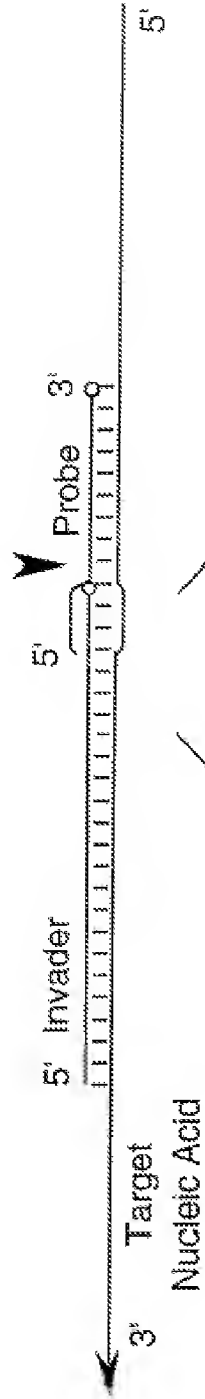
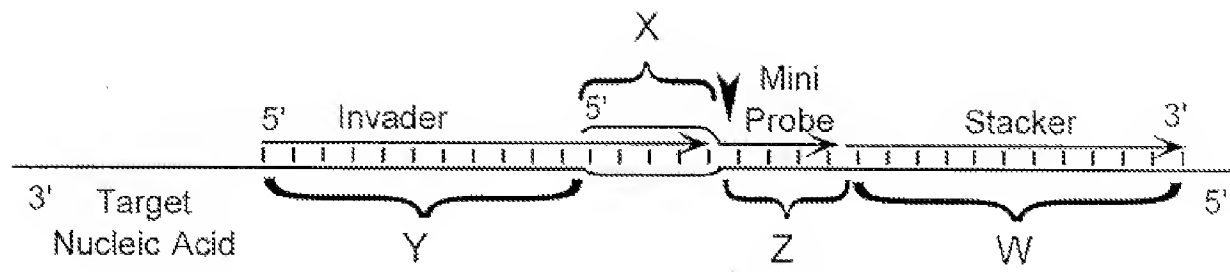


FIG. 56

FIGURE 68



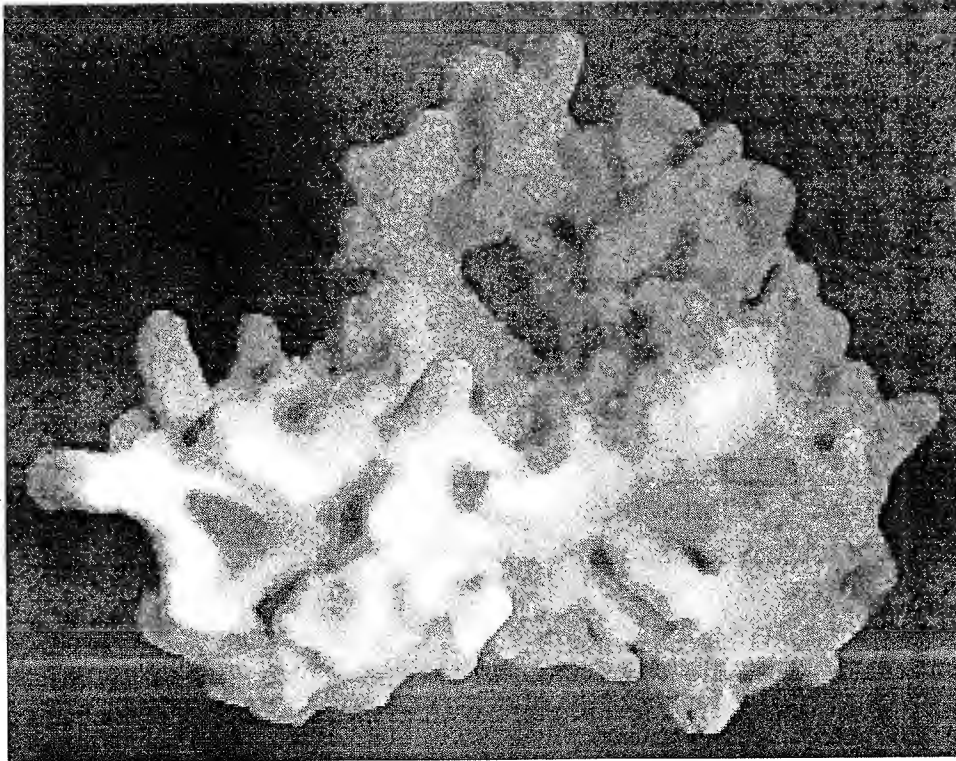


FIGURE 69

FIGURE 70 A

	10	20	30	40	50	60	70			
1	MGVQ----	FGDFIPK--	NIISFEDL	KGKKVAID	GMNALYQF	LTSIRLRD	SGSPLNRK	GEITSAYNGVFY	MJAFEN1.PRO	
1	MGVP-----	IGEIIPR--	KEIELENL	YGKKIAID	ALNAIYQF	LSTIRQKD	GTPLMDSK	GRITSHLSGLFY	PFUFEN1.PRO	
1	MGIQGLAKLI	ADVAPSAI	RENDIKSY	FGRKVAID	ASMSIYQF	LIAVRQ--	GGDVLQNEE	GETTSHLMGMFY	HUMFEN1.PRO	
1	MGIHGLAKLI	ADVAPSAI	RENDIKSY	FGRKVAID	ASMSIYQF	LIAVRQ--	GGDVLQNEE	GETTSHLMGMFY	MUSFEN1.PRO	
1	MGIKGLNAII	SEHVPSAI	RKSDIKS	FFGRKVAID	ASMSLYQF	LIAVRQ	QDGGQLTNEA	GETTSHLMGMFY	YST510.PRO	
1	MGVHSFWDI	AG----	PTARPVRL	ESLEDKRMA	VDASIIWIYQF	LKAVRDQ	EGNAVKN--	-----	SHITGFFR	YSTRAD2.PRO
1	MGVSGLWNIL	-----	PVKRPVKL	ETLVNKR	LAIIDASIIWIYQF	LKAVRD	KEGNQKLS	-----	SHVVGFFR	SPORAD13.PRO
1	MGVQGLWKLE	-----	CSGROVS	PEALEGKIL	AVDISIWL	NQALKGV	RDRHGN	SIEN-----	PHLLTLFH	HUMXPG.PRO
1	MGVQGLWKLE	-----	CSGHRVS	PEALEGKVL	AVDISIWL	NQALKGV	RDSHG	NVIEN-----	AHLLTLFH	MUSXPG.PRO
1	MGVQGLWKLE	-----	CSGRPIN	PGTLEKIL	AVDISIWL	NQAVKGA	RDRQGN	AIQN-----	AHLLTLFH	XENXPG.PRO
1	MTINGIWEWA	NHVV----	RKVPNET	MRDKT	LSIDGHI	WLYESL	KGCEAH	HQQJT-----	PNSYLVTFFT	CELRAD2.PRO

	80	90	100	110	120	130	140				
64	KTIHLENDIT	PIWVFDGE	PPKLEK	TRKVRRE	MKKEAEL	KMKEAIKK	-----	EDFEEAAKYAKRVS	YLTP	MJAFEN1.PRO	
64	RTINLMEAGI	KPVYVFDG	EPPEFKK	KELEKRR	EAREEAE	EKKWREALEK	-----	GEIEEARKYAQRAT	RVNE	PFUFEN1.PRO	
70	RTIRMMENG	IKPVYVFD	GKPPQLK	SGELAKR	SERRAEAE	EKKLQQAQA	-----	GAEOEVEKFTKRL	VKVT	HUMFEN1.PRO	
69	RTIRM-ENG	IKPVYVFD	GKPPQLK	SGELAKR	SERRAEAE	EKKLQQAQA	-----	GMEEEVEKFTKRL	VKVT	MUSFEN1.PRO	
71	RTLRMIDNG	IKPCYVFD	GKPPDLK	SHELTKR	SSRRVET	EKKLA--EA--	-----	TTELEKMKQERR	LKVSK	YST510.PRO	
61	RICKLLYFG	IRPVVFDG	GVPLK	RETIRQ	RKERRQ	GKRESAK	STARKLLALQ	LQNGSNDN	KRDSDEV	TM	YSTRAD2.PRO
61	RICKLLFFG	IKPVVFDG	GAPSLK	RQTIQ	KRQARR	LDRREENA	TVTANKLLALQ	MRHQAML	KRDADEV	TQ	SPORAD13.PRO
61	RLCKLLFFR	IRPIFVFDG	DAPLLK	QTLVKR	RQRKD	LASSDSR	KTTTEKLLK	TFLKRAI	KTERIAA	TVTG	HUMXPG.PRO
61	RLCKLLFFR	IRPIFVFDG	DAPLLK	QTLAKR	RQRKDS	ASIDS	SRKTTTEKLLK	TFLKRAI	KTDRIA	ASVTG	MUSXPG.PRO
61	RLCKLLFFR	IRPIFVFDG	EAPLLK	RQTLAK	RQRRT	TKASND	ARKTNEKLL	RTFLKRAI	KAERIAA	TVTG	XENXPG.PRO
60	RIORILLEKI	PIVVF	DNINASSA	HESKDQNE	FVPRKRRS	FGDSPFTNI	V-----	-----	-----	-----	CELRAD2.PRO

FIGURE 70 B

	150	160	170	180	190	200	210
130	KMVENCKYLLSLMGIPYVEAPSEGEAQAASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTTKEM----						MJAFEN1.PRO
130	MLIEDAKKLLLELMGIPVQAPSEGEAQAAYMAAKGSVYASASQDYDSLFGAPRLVRNLTTGKRKLPGK						PFUFEN1.PRO
136	QHNDCKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPQ						HUMFEN1.PRO
134	QHNDCKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPQ						MUSFEN1.PRO
134	EHNEEAQKLLGLMGIPYIIAPTAEAAQCAELAKKGKVYAAASEDMOTLCYRTPFLRLRHLTFSEAKKEPIH						YST510.PRO
131	DMIKEVQELLSRFGIPYITAPMEAEQAQCAELLQLNLVDGIITDDSOVFLFGGTKIYKNMFHEKNY----						YSTRAD2.PRO
131	VMIKECQELLRLFGIPYIVAPOEAEQAQCSKLELKLVDGIVTDDSOVFLFGGTRVYRNMFNQKFN----						SPORAD13.PRO
131	QMFLESQELLRLFGIPYIQAPMEAEQAQCAILDITDQTSGTITDDSDIWLFGARHVYRNFNKNKF----						HUMXPG.PRO
131	QMFLESQELLRLFGVPIYIQAPMEAEQAQCAVLDSLQTSGTITDDSDIWLFGARHVYKFNKNKF----						MUSXPG.PRO
131	QMCLESQELLQLFGIPYIVAPMEAEQAQCAILDITDQTSGTITDDSDIWLFGARHVYKNFFSQNKH----						XENXPG.PRO
111	OHVYKTNALLTELGIKVI IAPGDGEAQCARLEQLQGVTS6CITTDYFDYFLFGKNLYRDEFTAGT-----						CELRAD2.PRO
	220	230	240	250	260	270	280
195	-----PELIELNEVLEDLRISLQDLIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV						MJAFEN1.PRO
200	NVYVE-IKPELIIIEEVKELKLTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF						PFUFEN1.PRO
206	EFHLSRILQELGLNQEQFVDLCILLGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLDPN----						KY HUMFEN1.PRO
204	EFHLSRVLQELGLNQEQFVDLCILLGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLDPS----						KY MUSFEN1.PRO
204	EIDTELVLRLGLDLTIEQFVDLCIMLGCDYCESIRGVGPVTALKLIKT--HGSIEKIVEFIESGESNNTKW						YST510.PRO
198	FYDAESI LKLLGLDRKNMIELAQLLGSDYTNGLKMGMPVSSIEVIAEF--GNLKNFKDWNNGOFDKRK						YSTRAD2.PRO
198	LYLMDDMKREFNVNQMDLIKLAHLGSDYTMGLSRVGPVLALEILHEFPDGTGLFEKKWFQRLSTGHAS						SPORAD13.PRO
198	YYQYVDFHNLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPCHGLEPLLKFSEWWHEAQKNP						HUMXPG.PRO
119	YYQYVDFYSQGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPGRGLDPLLKFEWWHEAQNNK						MUSXPG.PRO
198	YYQYADIHNOLGLDRSKLINLAYLLGSDYTEGIPTVGVYSAMEILNEFPQGGLLEPLVKFEWWSEAQKDK						XENXPG.PRO
175	-----SSTACLHIDIMHLSLGRMF-----						CELRAD2.PRO

FIGURE 70 C

	290	300	310	320	330	340	350
251	LKKEVEYYDEIKRIFKEPKV	-----	-----	-----	-----	-----	MJAFEN1.PRO
265	QKQSDVDLYAIKEFFLNPPV	-----	-----	-----	-----	-----	PFUFEN1.PRO
269	PVPENWLHKEAQLFLEPEV	-----	-----	-----	-----	-----	HUMFEN1.PRO
267	PVPENWLHKEAQLFLEPEV	-----	-----	-----	-----	-----	MUSFEN1.PRO
272	KIPEDPYKQARMFLDPEV	-----	-----	-----	-----	-----	YST510.PRO
265	QETENKFEKDLRKKLVNNEI	ILDDDFPSVMVYDAYMRPEV	-----	-----	-----	-----	YSTRAD2.PRO
268	KNDVNTPVKKRINKLVGK	-IILPSEFPNPLVDEAYLHPAVDDSKQSFQWGI	PDLDLDELQFLMATVGSQ	-----	-----	-----	SPORAD13.PRO
268	KIRPNPHDTKVKKKL	--RTLQLTPGFPNPAVAEAYLKPVVDOSKGSFLWGGK	PDLDKIREFCORYFGWNRT	-----	-----	-----	HUMXPG.PRO
268	KVAENPYDTKVKKKL	--RKLQLTPGFPNPAVADAYLRPVVDDSRGSLWGGK	PDVDKIREFCORYFGWNRM	-----	-----	-----	MUSXPG.PRO
268	KMRPNPNDTKVKKKL	--RLDLQQSFNPAVASAYLKPVVDESASFSWGRPD	LEQIREFCESRFGWYRL	-----	-----	-----	XENXPG.PRO
194	-----EKKVSRPHLISTAIL	LGCDYFORGVQNI	GIVSVFD-ILGEFGD	CNNEIDPHVILDRFASVRE	-----	-----	CELRAD2.PRO
	360	370	380	390	400	410	420
300	RVKKHVDKLYNLIA	-----	-----	-----	-----	-----	MJAFEN1.PRO
314	RVKNGLERLKKAI	-----	-----	-----	-----	-----	PFUFEN1.PRO
320	RIRSGVKRISKSQGS-TQGR	LDFFKVT	-----	-----	-----	-----	HUMFEN1.PRO
318	RIRSGVKRISKSQGS-TQGR	LDFFKVT	-----	-----	-----	-----	MUSFEN1.PRO
323	RVKSGISRLLKGLKSG-IQGR	LDGFFOVV	-----	-----	-----	-----	YST510.PRO
335	KSDEILPLIRDVNKRKK	-----	-----	-----	-----	-----	YSTRAD2.PRO
337	RTNEVLLPVIQDMHKKOF	-----	-----	-----	-----	-----	SPORAD13.PRO
336	KTDSELPVLKQLDAQQTQLR	IDSFRLAQQEKEDAKRIKSQRLNRAVTCMLRKEKEA	AASEIEAVSVAM	-----	-----	-----	HUMXPG.PRO
336	KTDSELPVLKHLNAHQTLR	IDSFRLAQQEKQDAKLIKSHRLSRAVTCMLRKEEKE	KAPELTKVTEAM	-----	-----	-----	MUSXPG.PRO
336	KTDEVLPLVLKQLNAQQTQLR	IDSFRLAQQEKQDAKLIKSHRLSRAVTCMLRKEEKE	VEEVEAAVAM	-----	-----	-----	XENXPG.PRO
257	EIPARSEDQTKRLRLRRKKYNF	PVCGFPNCDAVHNAT	TMYL RPPVSSEIPKIIPR	-----	-----	-----	CELRAD2.PRO



FIGURE 70 E

322 DAWFKZ  
335 ESWFKR  
375 KFKRGK  
373 KFKRGK  
377 VTKGRR  
390 --RKM  
483 SKRRRK  
546 RKRKTZ  
538 RRKKKT  
523 TVRRK  
429 ELGDSO

MJAFEN1.PRO  
PFUFEN1.PRO  
HUMFEN1.PRO  
MUSFEN1.PRO  
YST510.PRO  
YSTRAD2.PRO  
SPORAD13.PRO  
HUMXPG.PRO  
MUSXPG.PRO  
XENXPG.PRO  
CELRA02.PRO



FIGURE 71

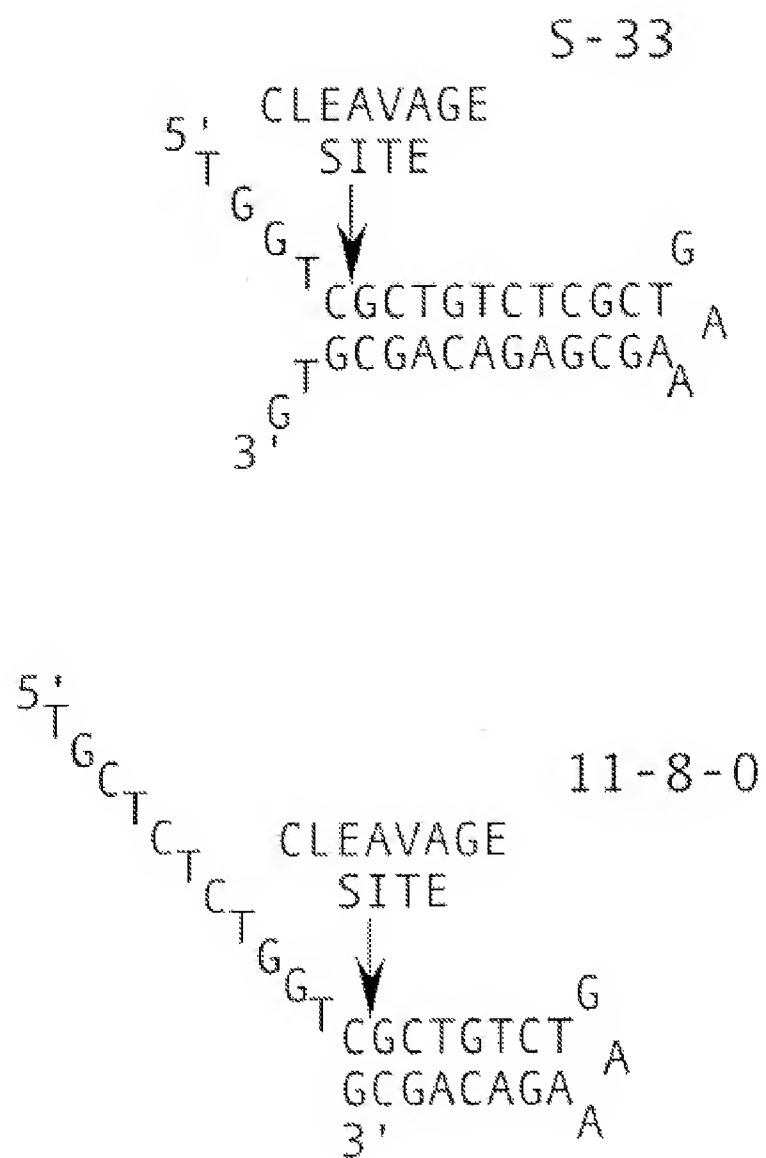


FIGURE 72

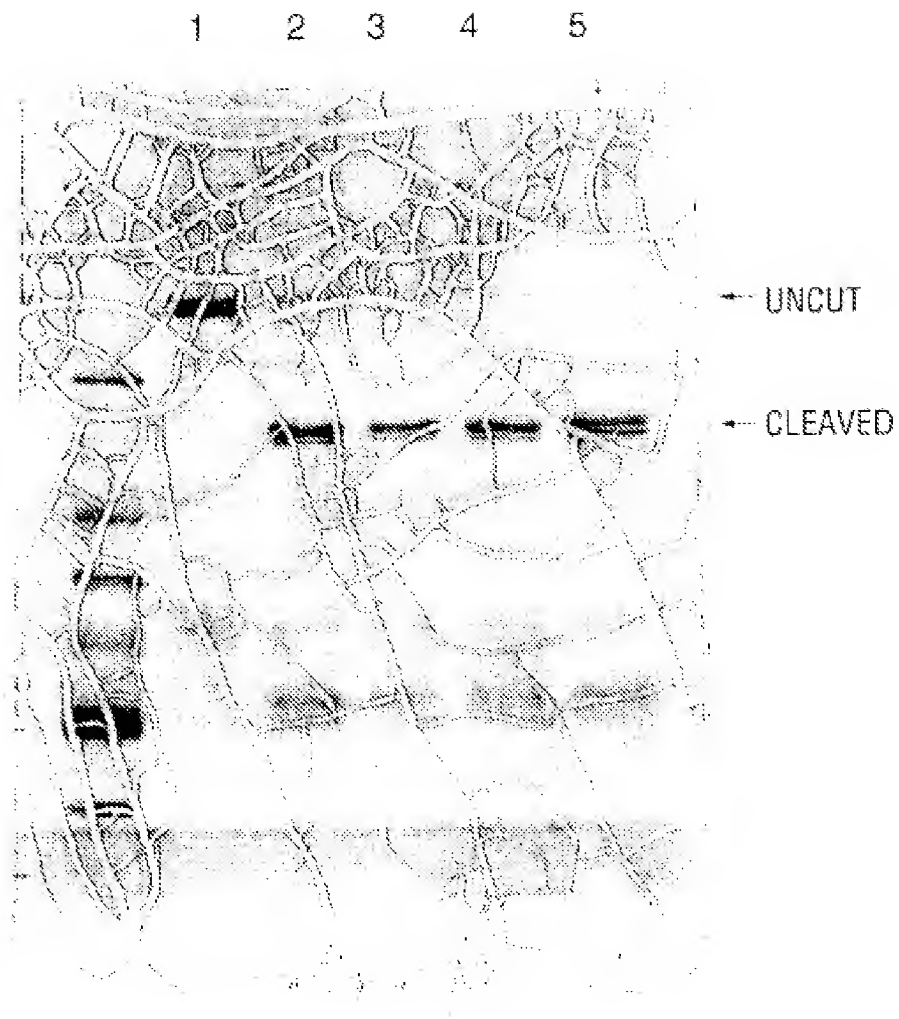


FIGURE 73

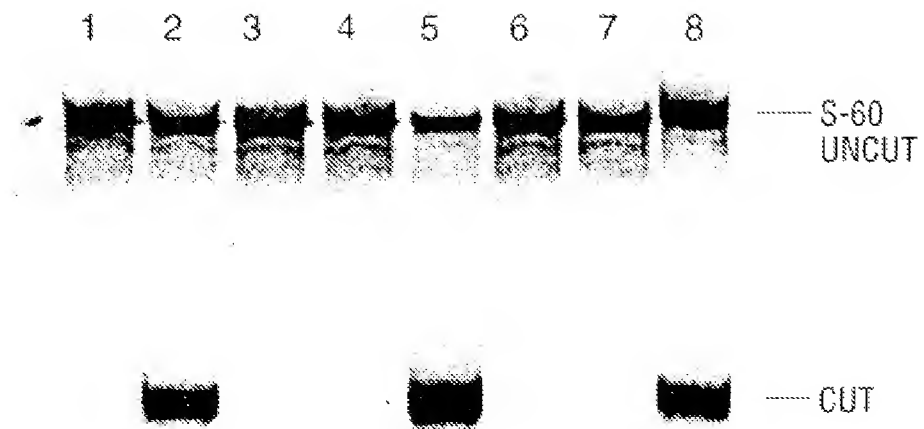


FIGURE 74

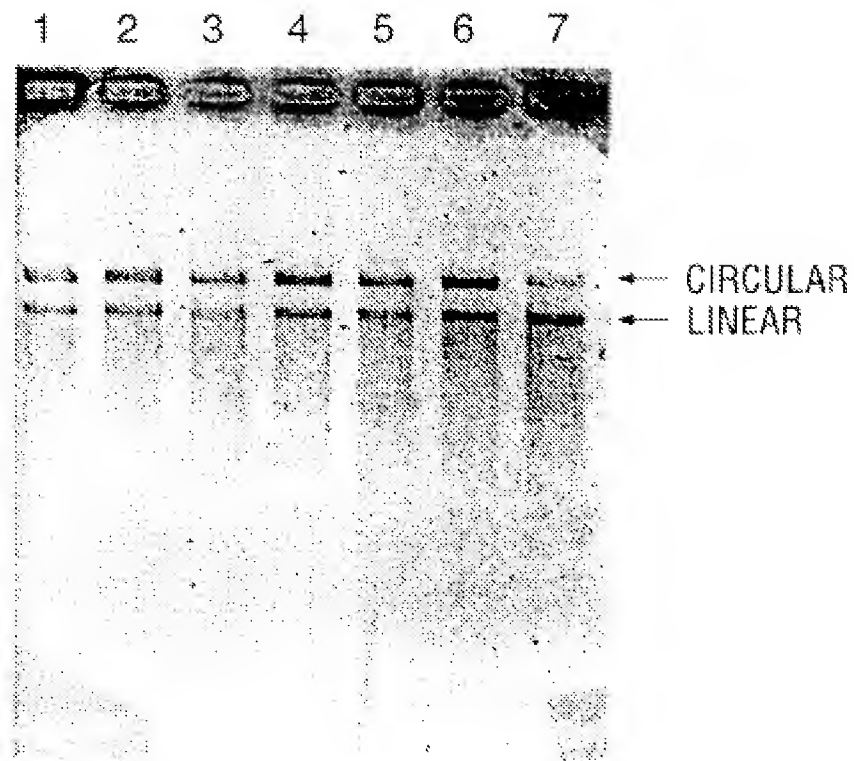


FIGURE 75

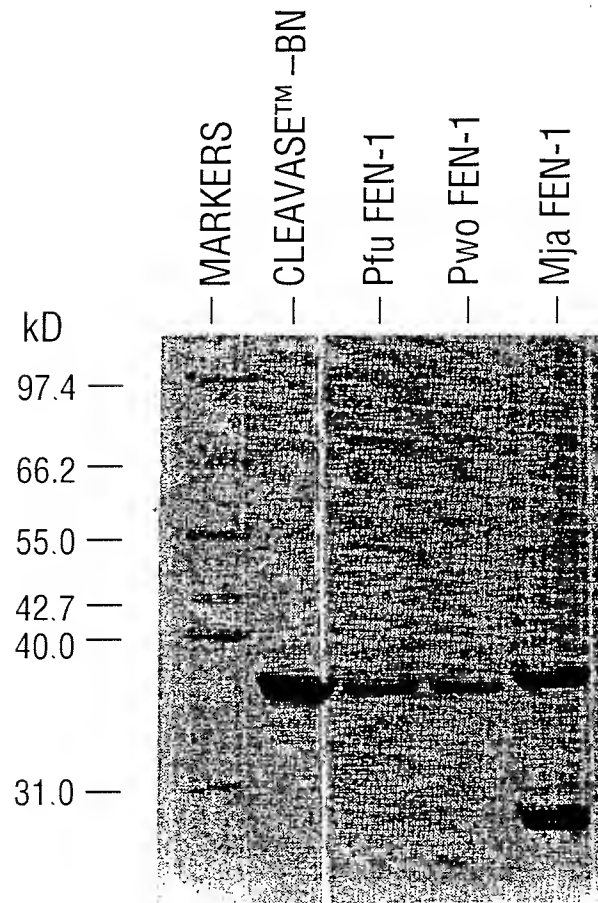


FIGURE 76

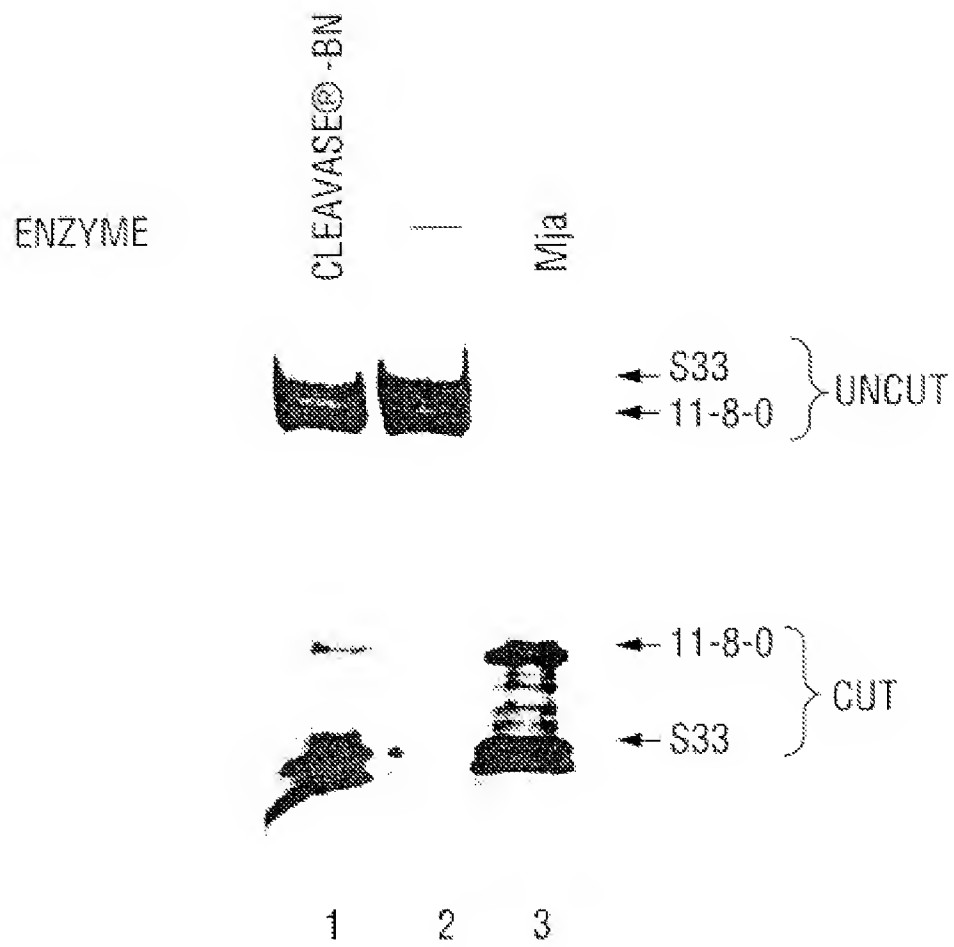


FIGURE 77

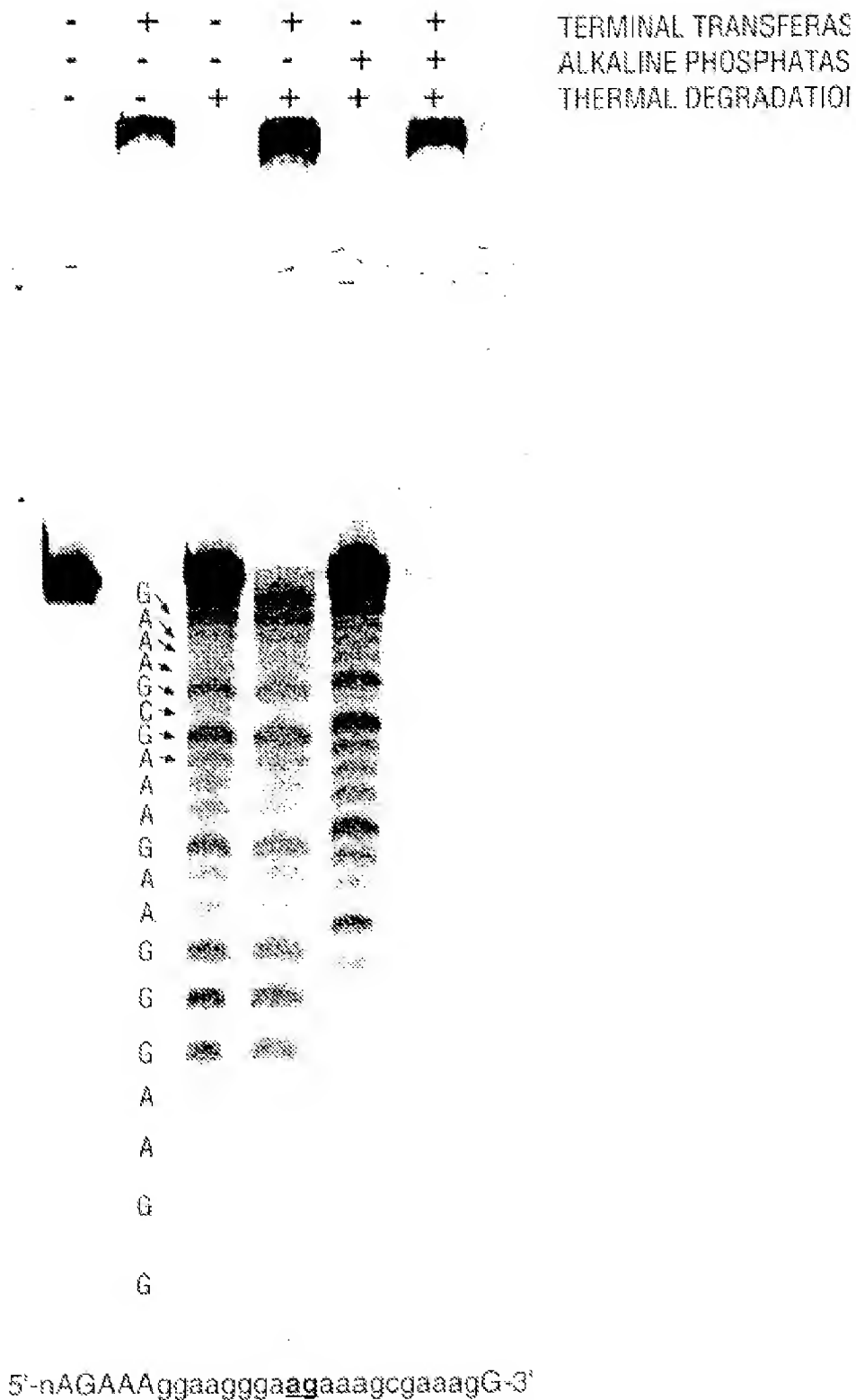
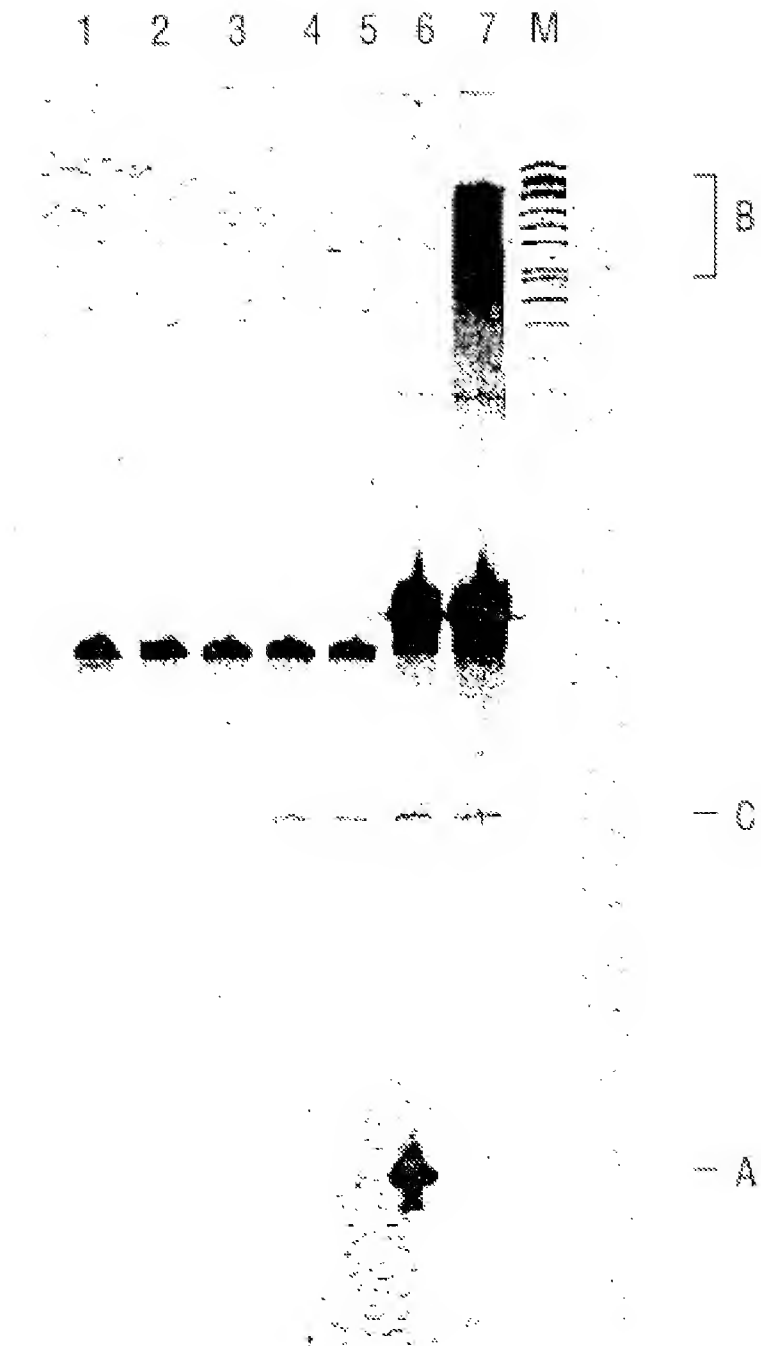


FIGURE 78





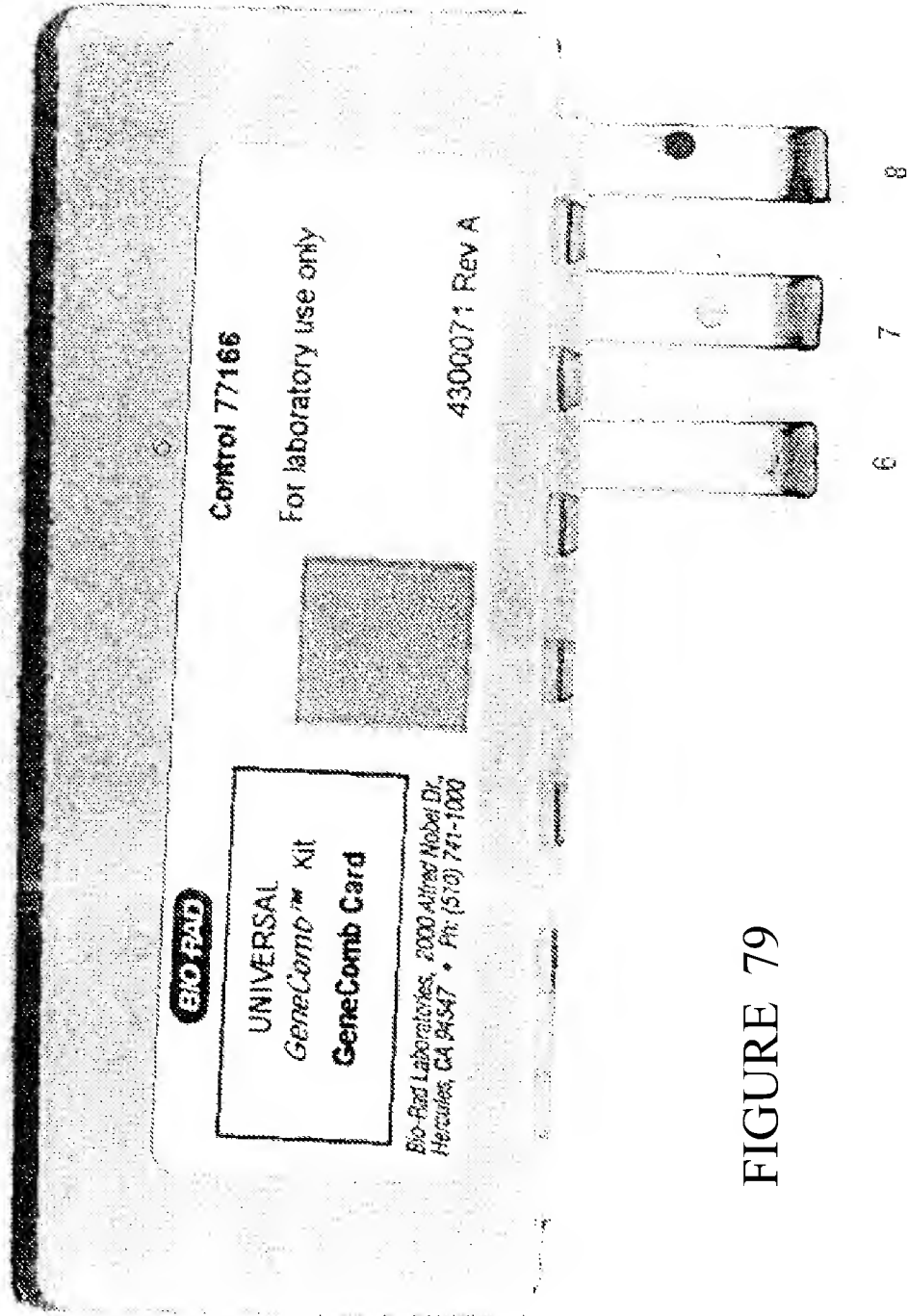


FIGURE 79

FIGURE 80

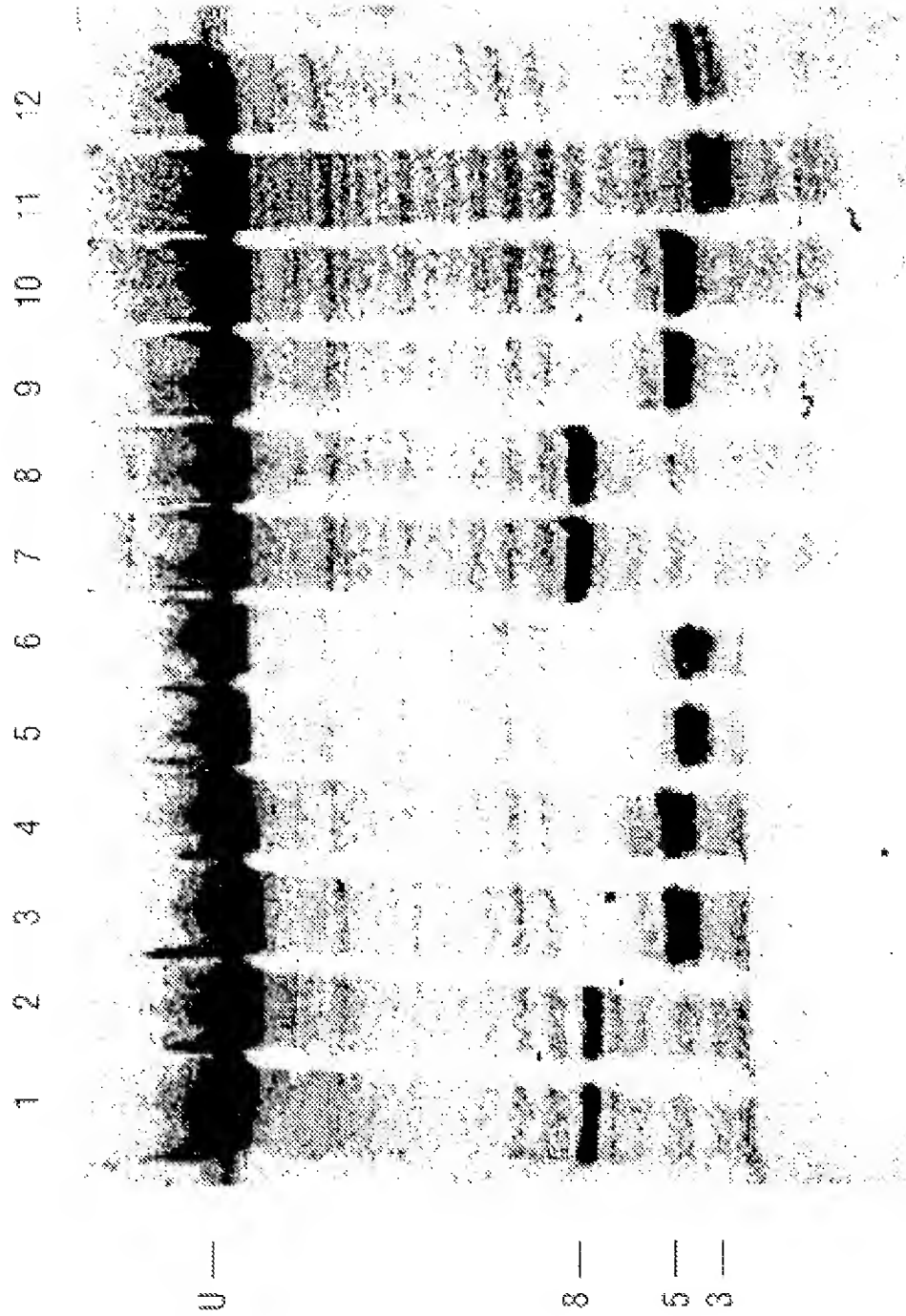


FIGURE 81

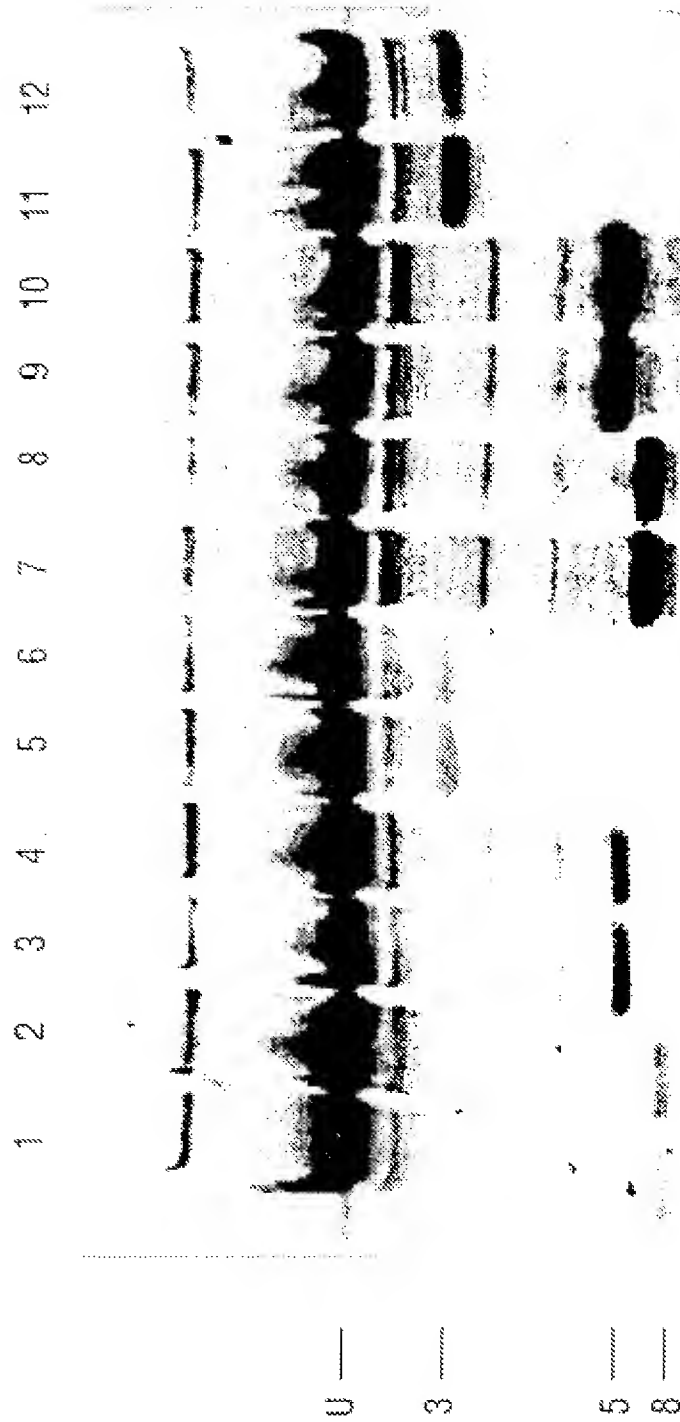


FIGURE 82

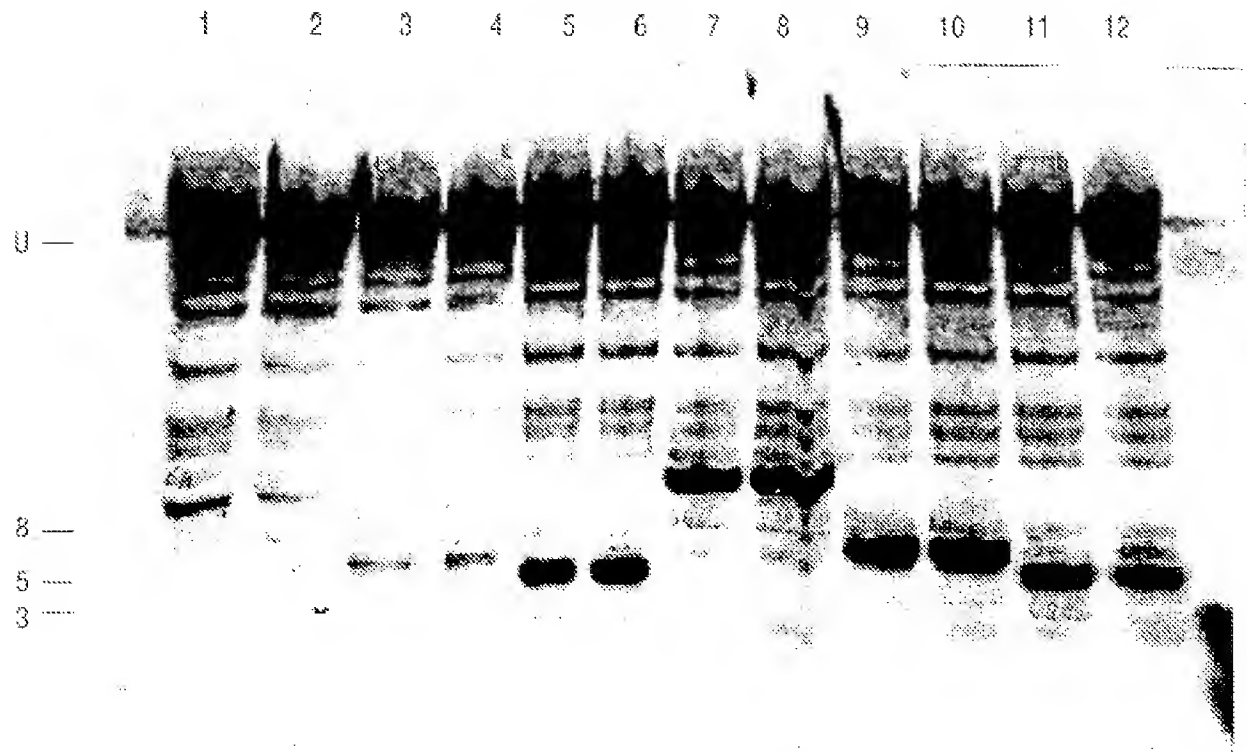


FIGURE 83

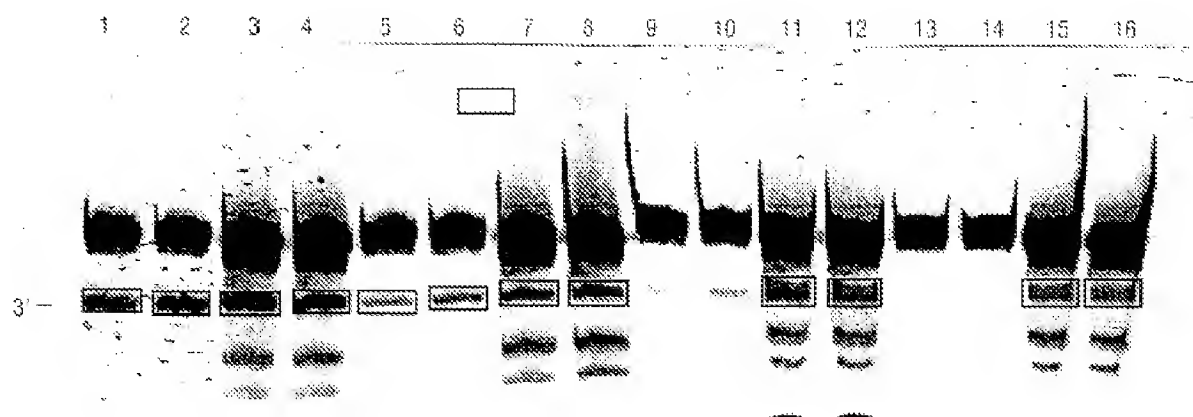
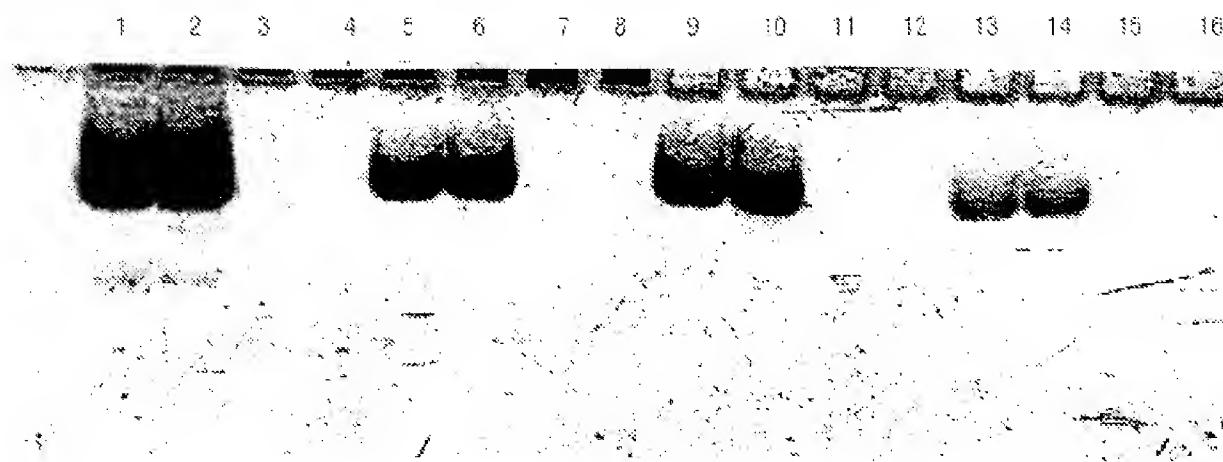
**A****B**

FIGURE 84

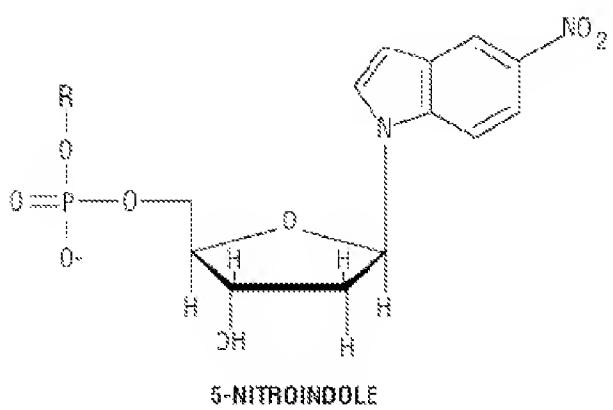
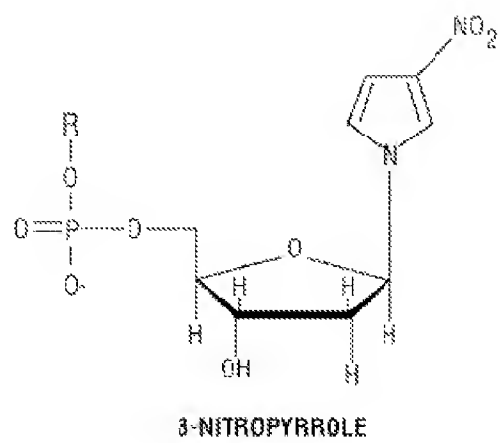


FIGURE 85

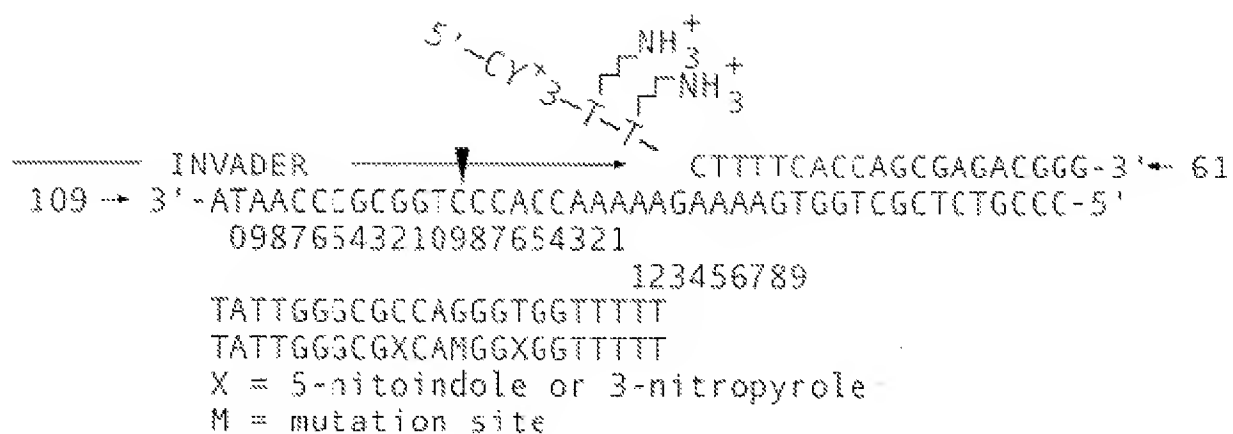
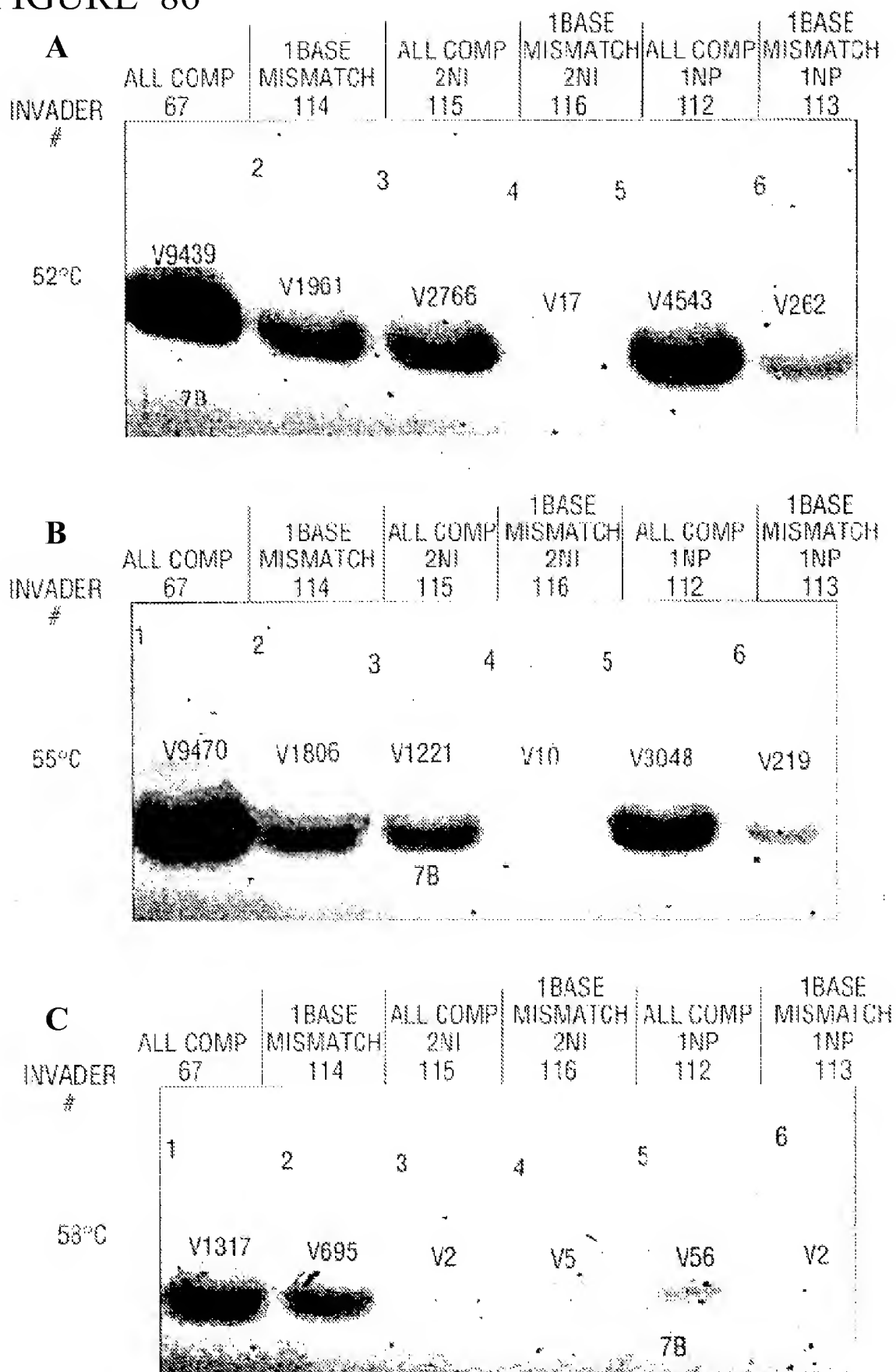


FIGURE 86





## FIGURE 87

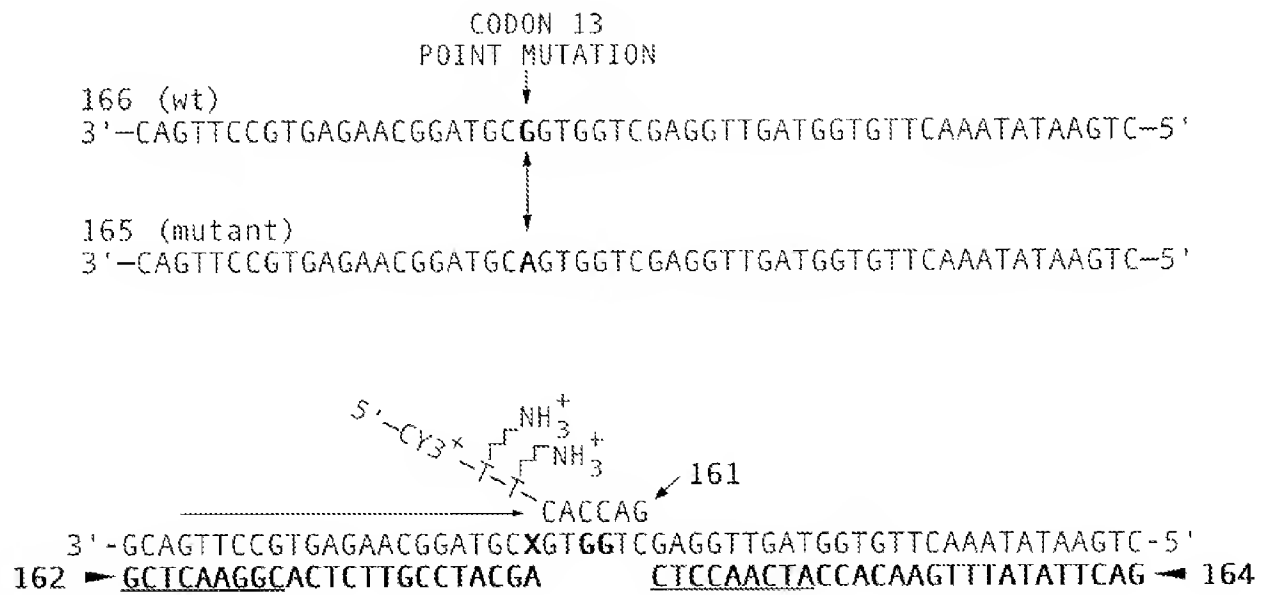


FIGURE 88

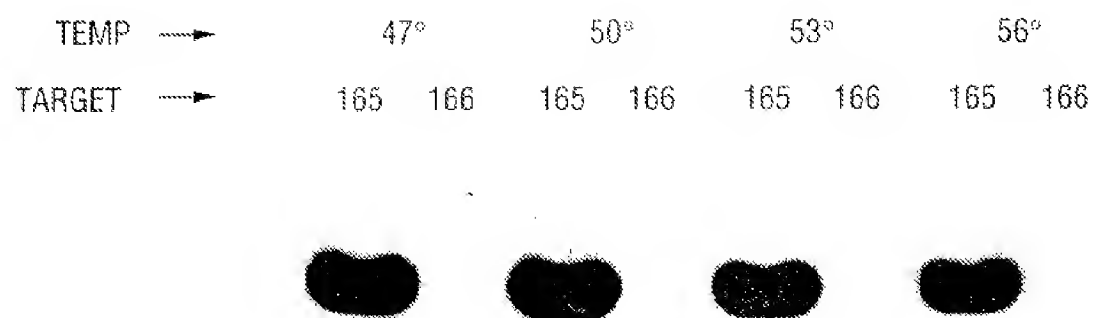


FIGURE 89

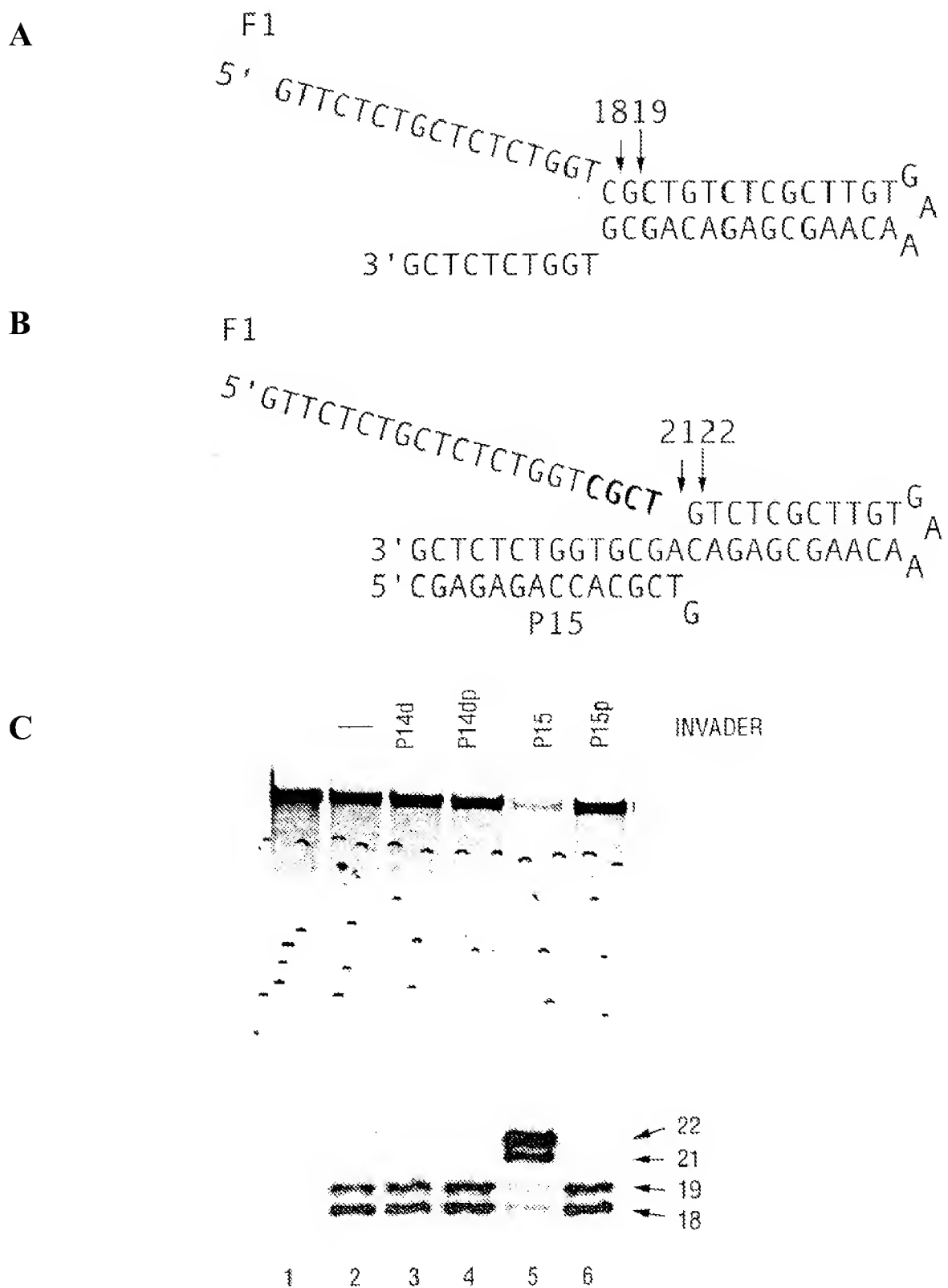


FIGURE 90

## Invader 3' -end Substituents

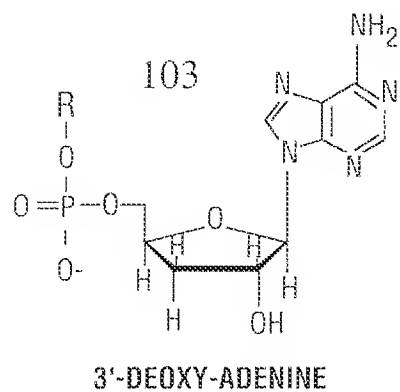
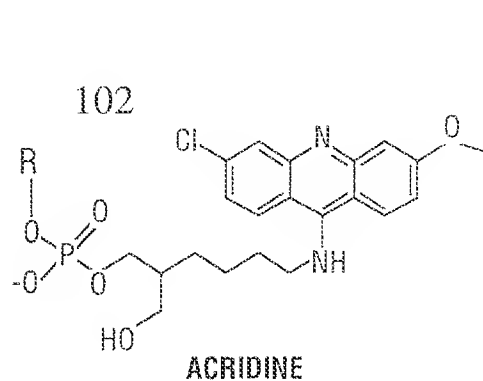
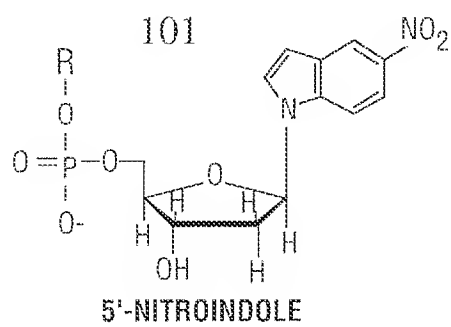
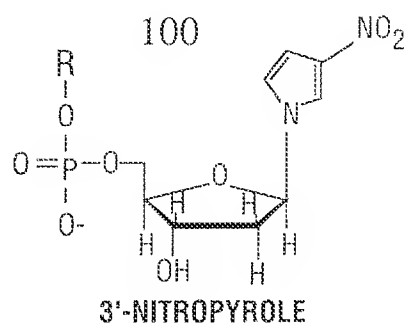
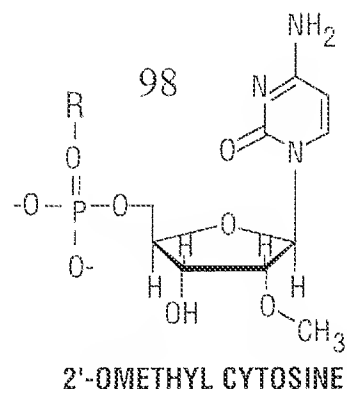
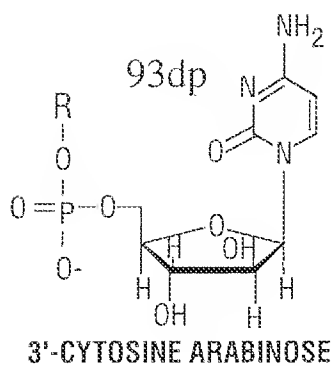
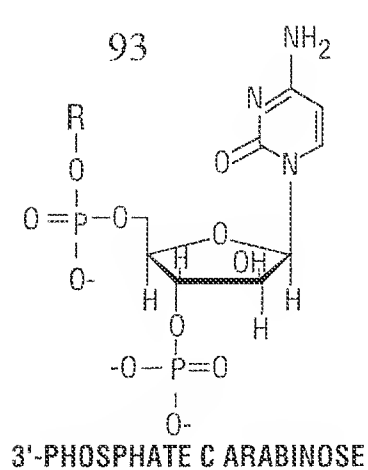
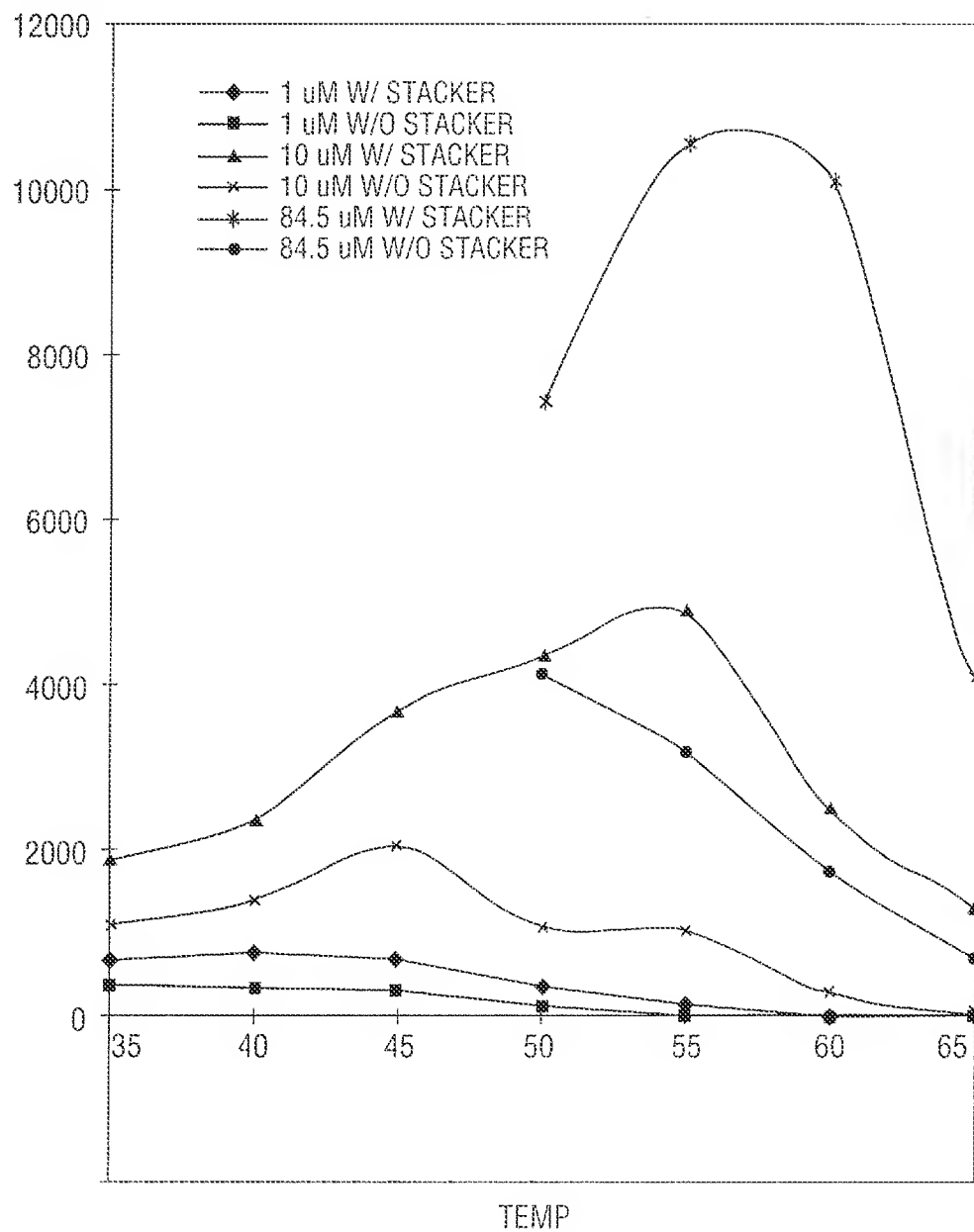


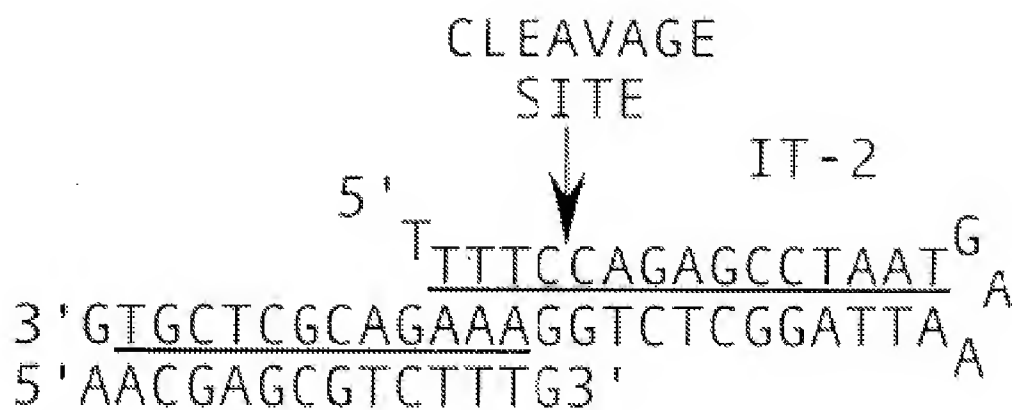
FIGURE 91

COUNTS

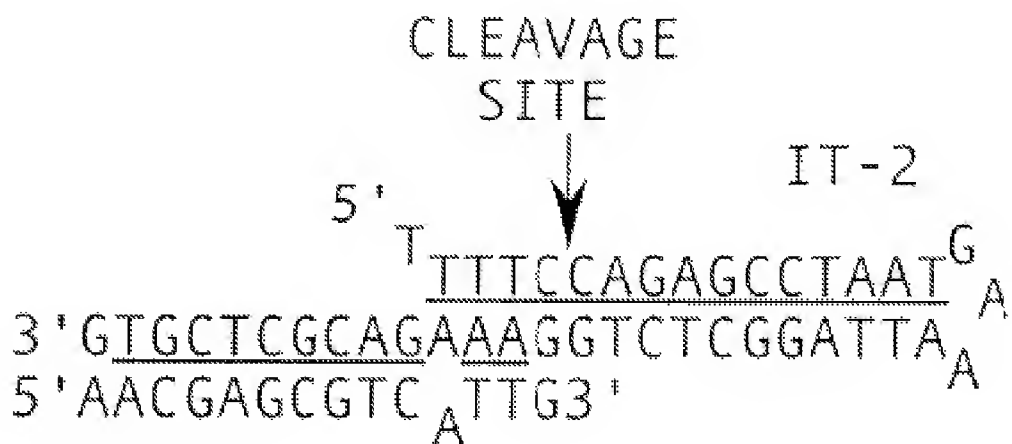


CONCENTRATION OF PROBE W/ AND W/O STACKER vs TEMP

FIGURE 92



IT-1



IT-1A4

FIGURE 93

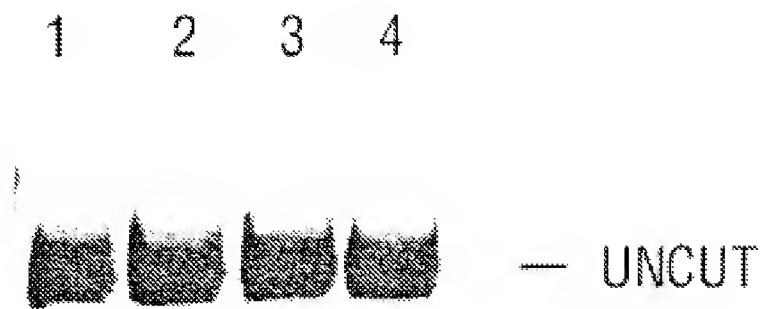


FIGURE 94

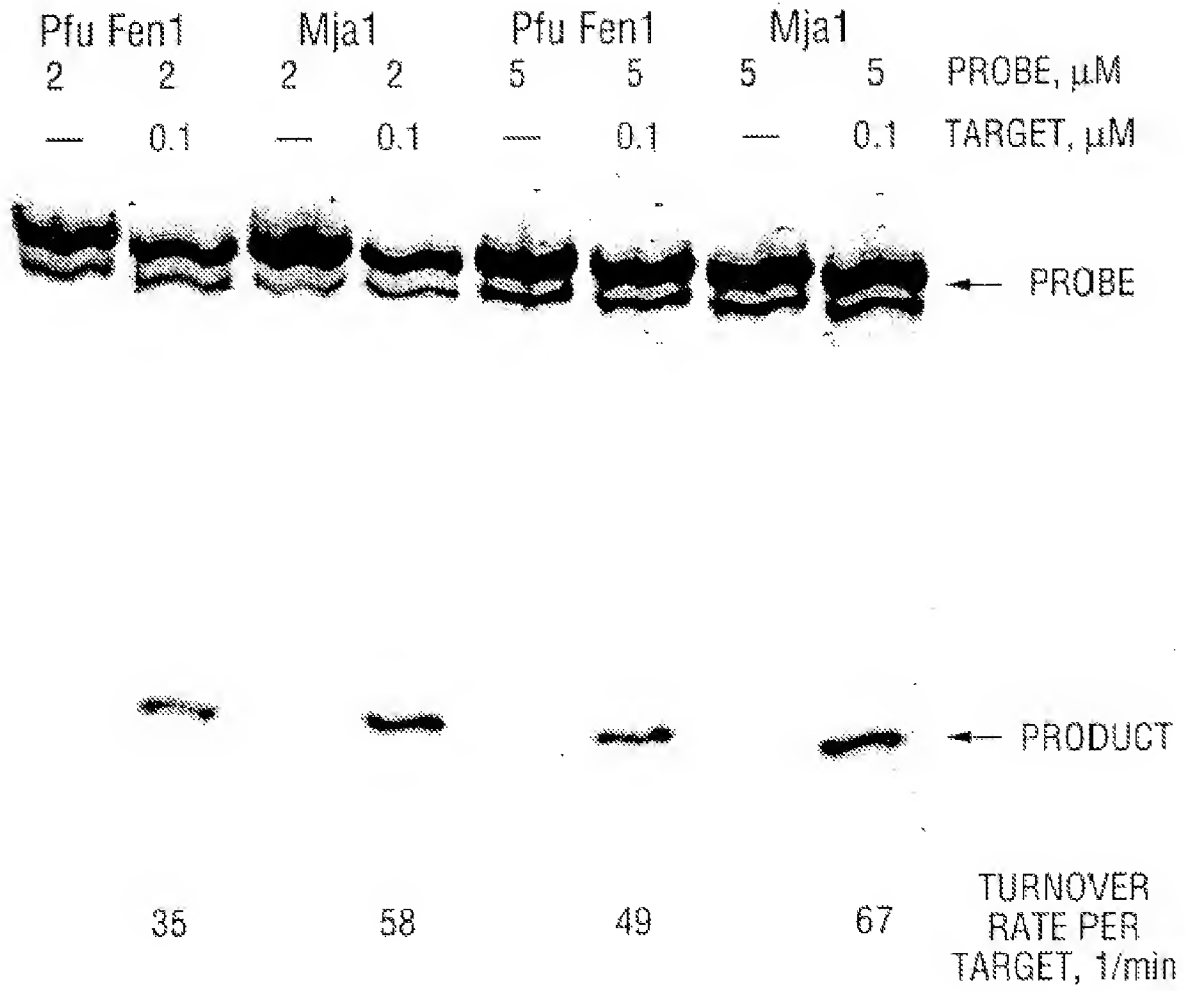




FIGURE 95

1 2 3 4 5

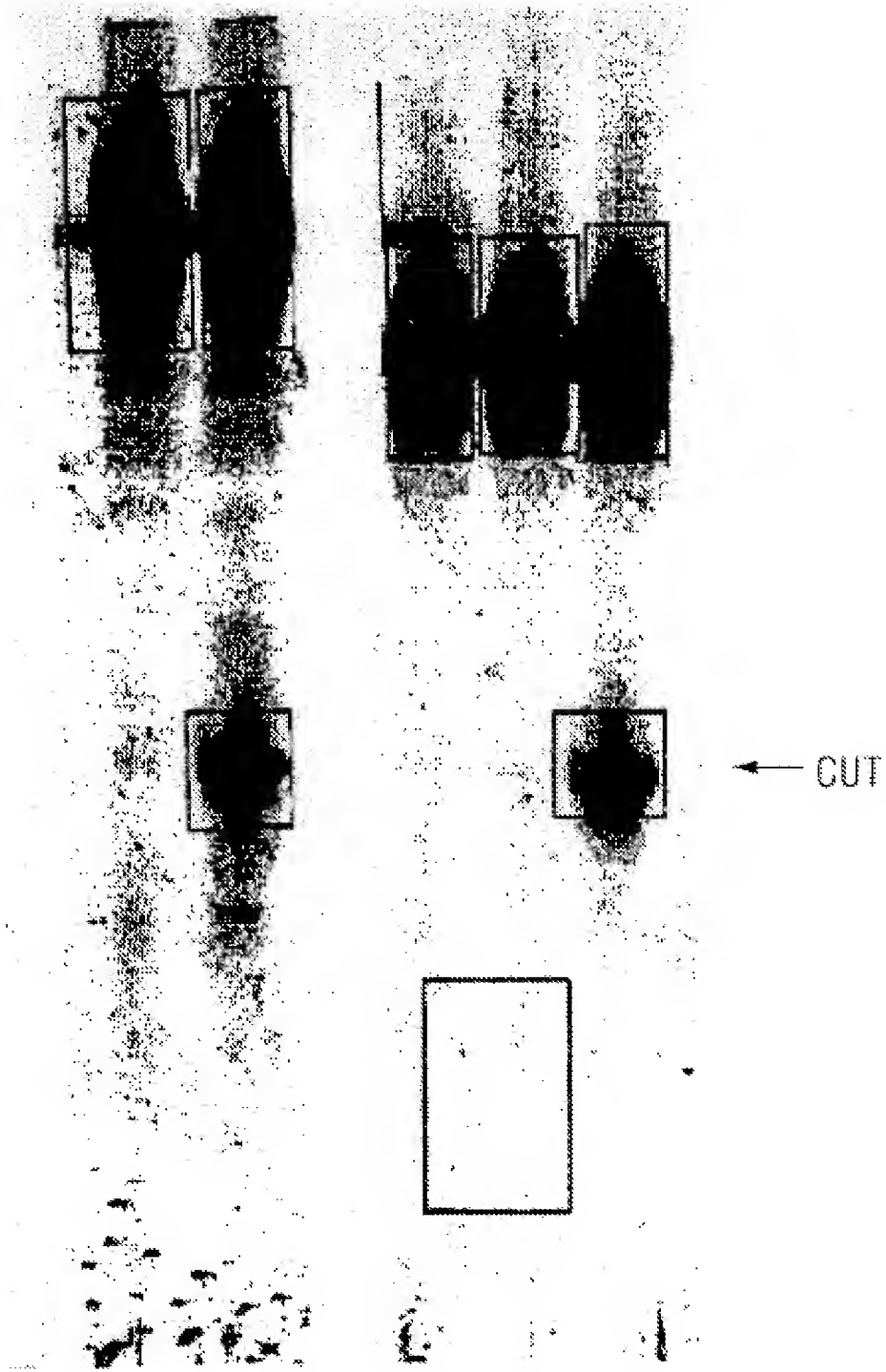
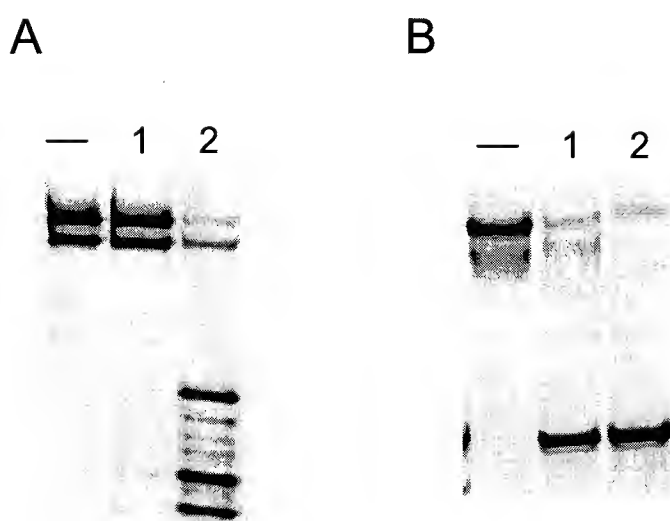


FIGURE 96



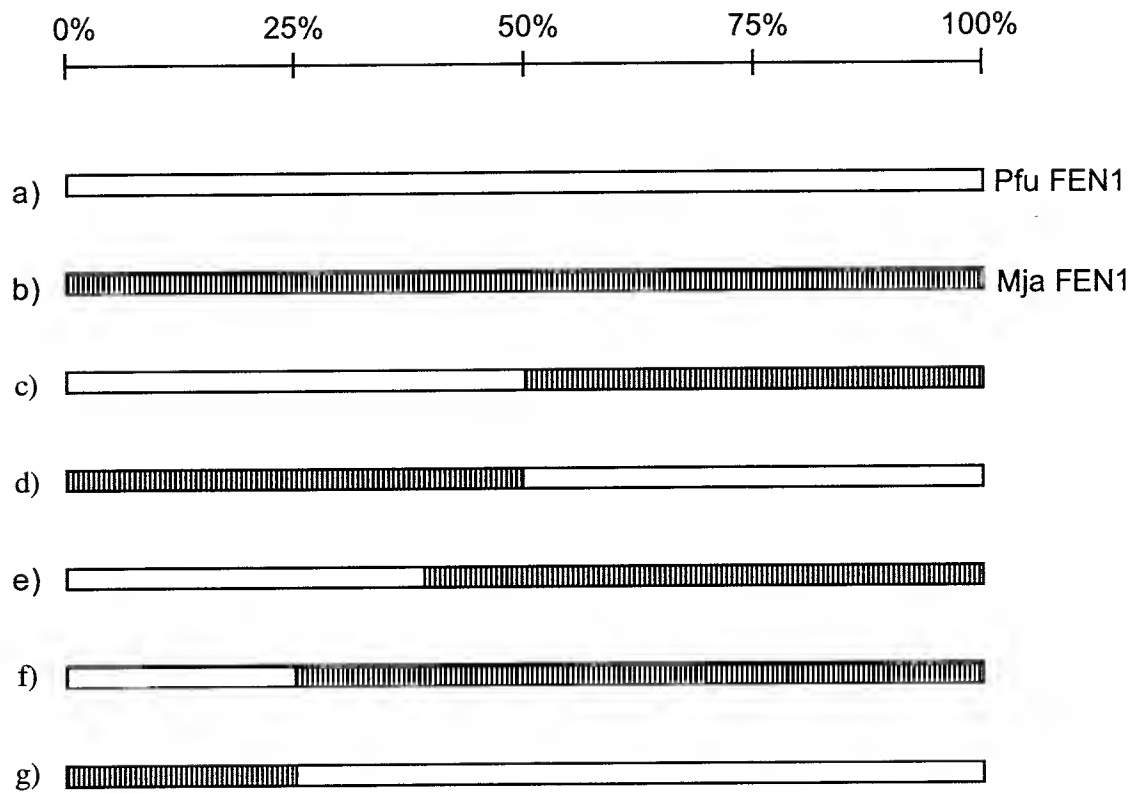
**FIGURE 97**

FIGURE 98A

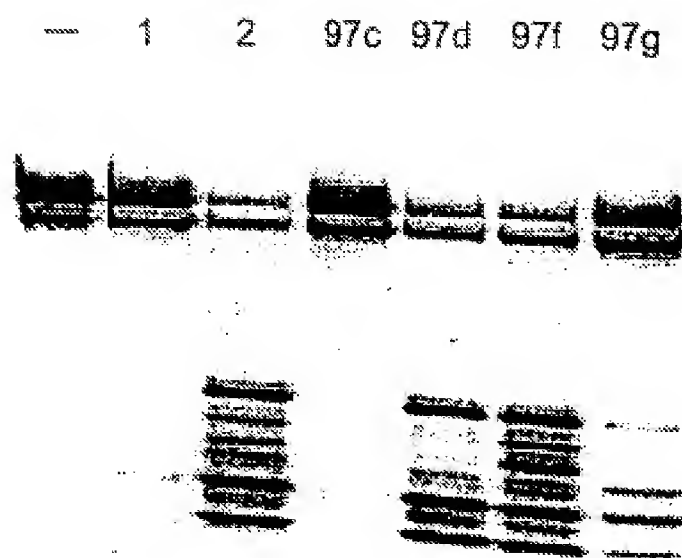


FIGURE 98B

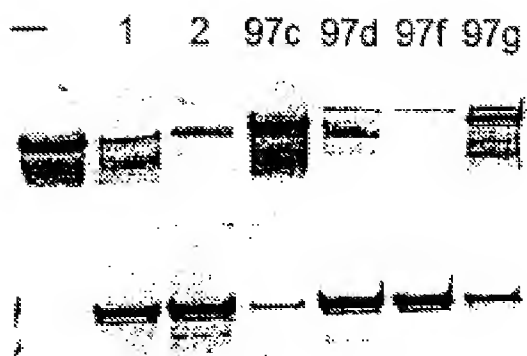
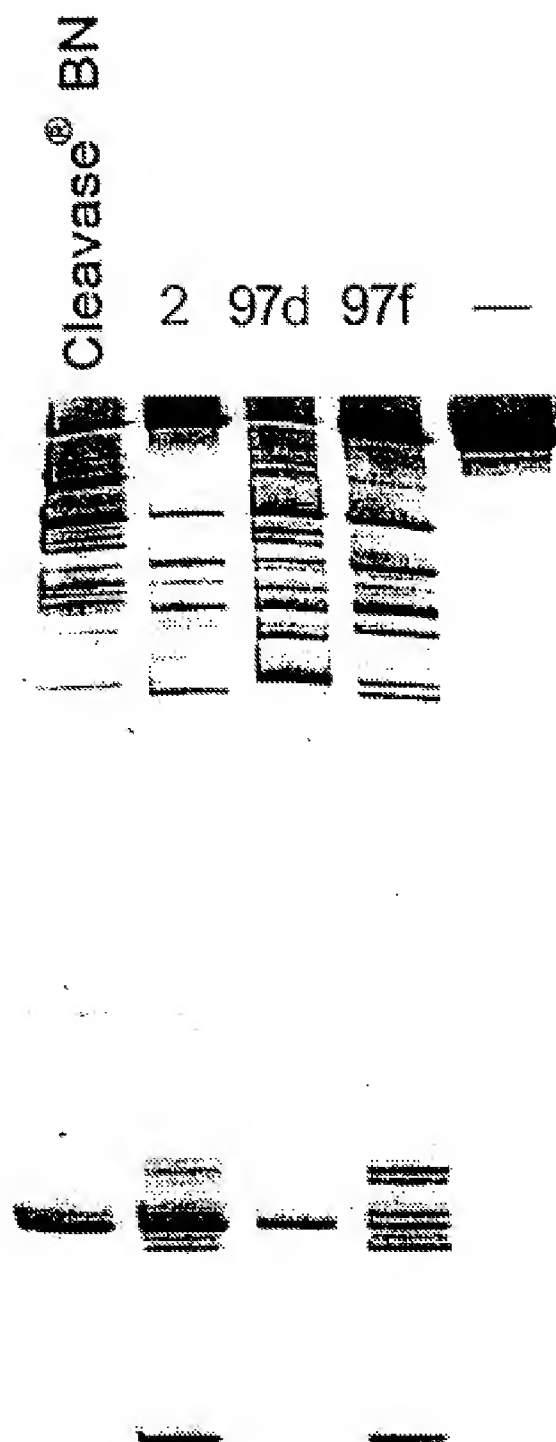
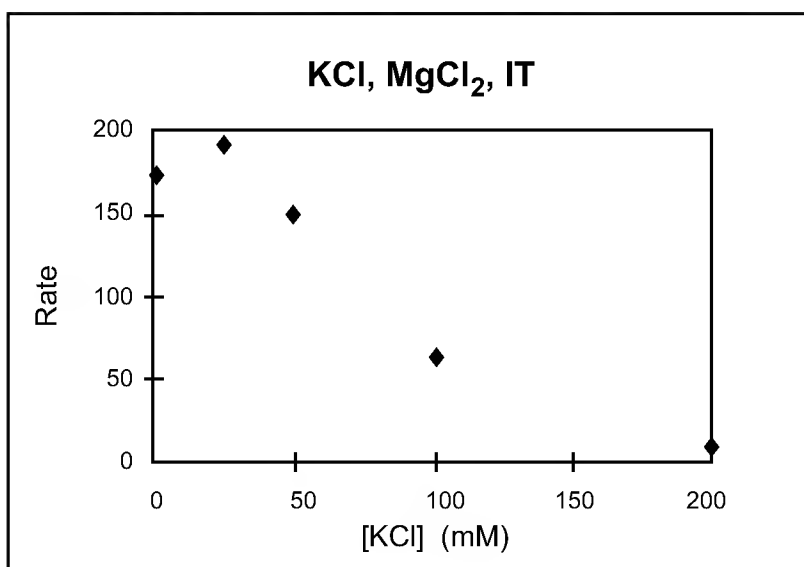
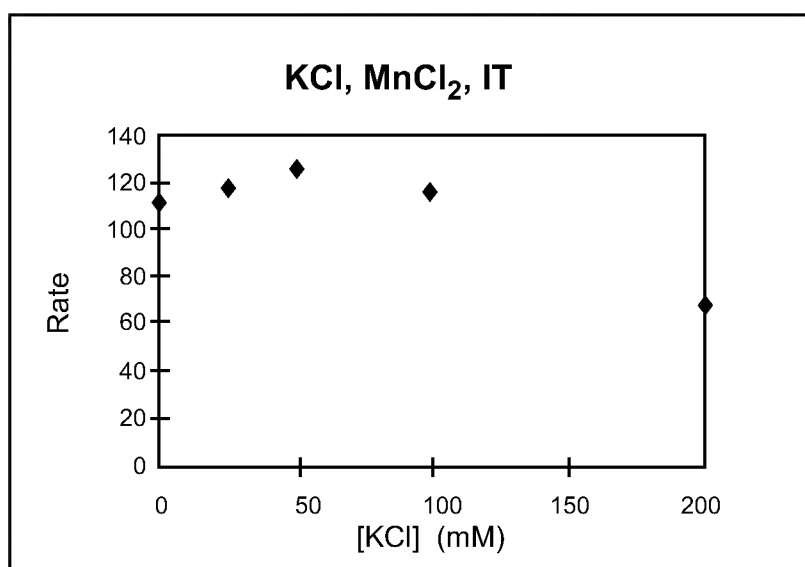


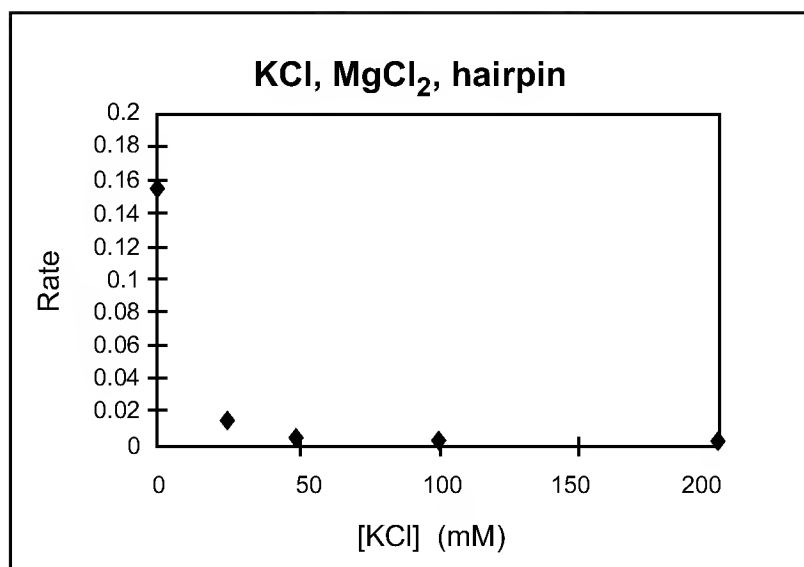
FIGURE 99

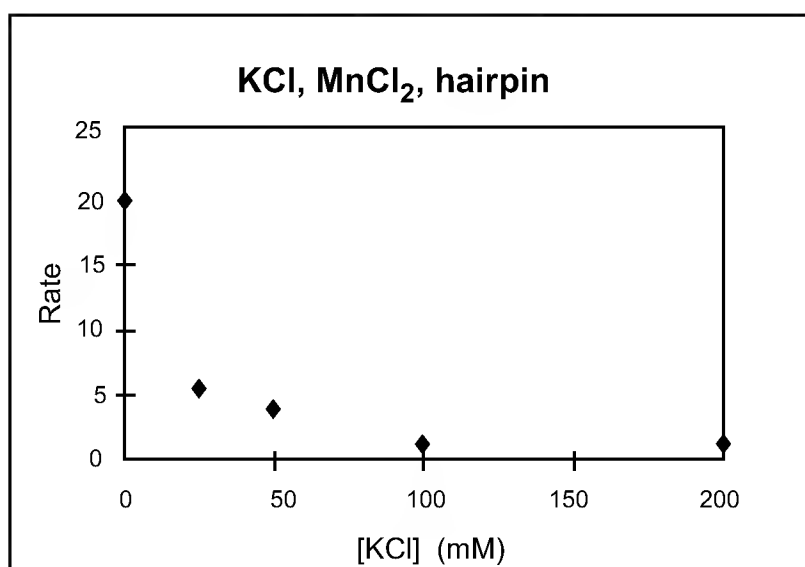


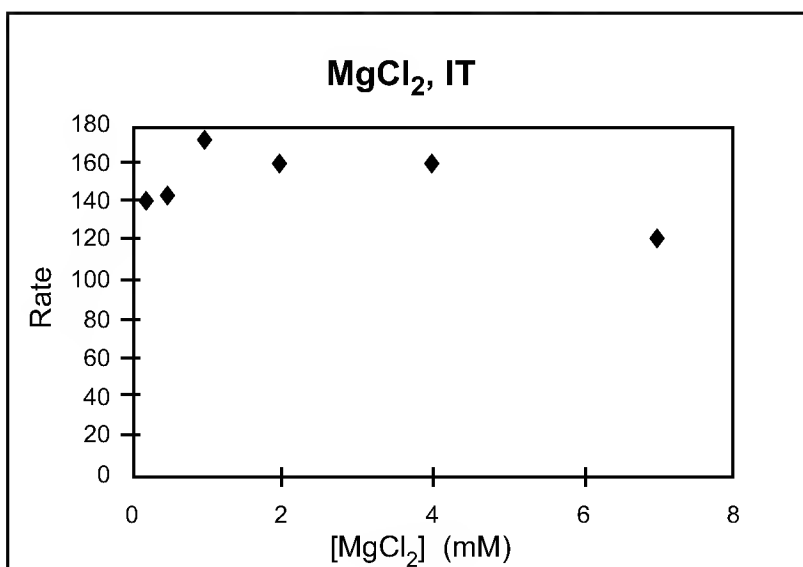
**FIG. 100A**

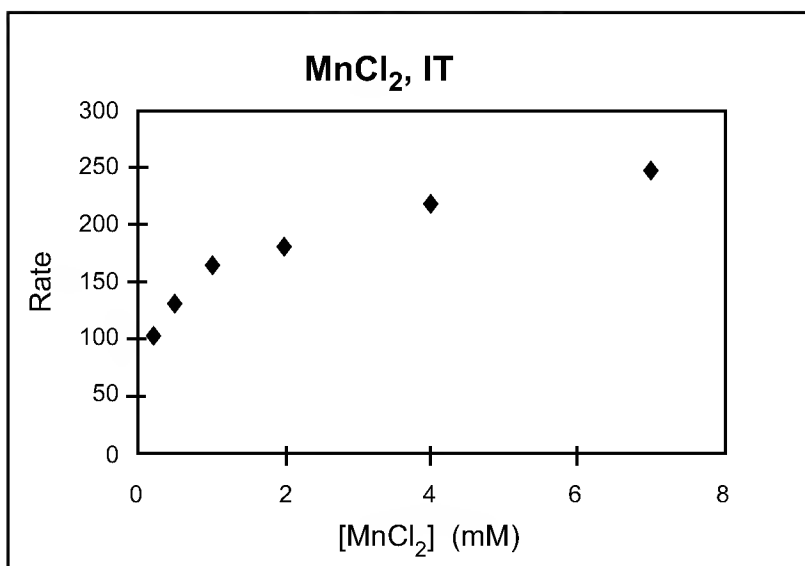
**FIG. 100B**

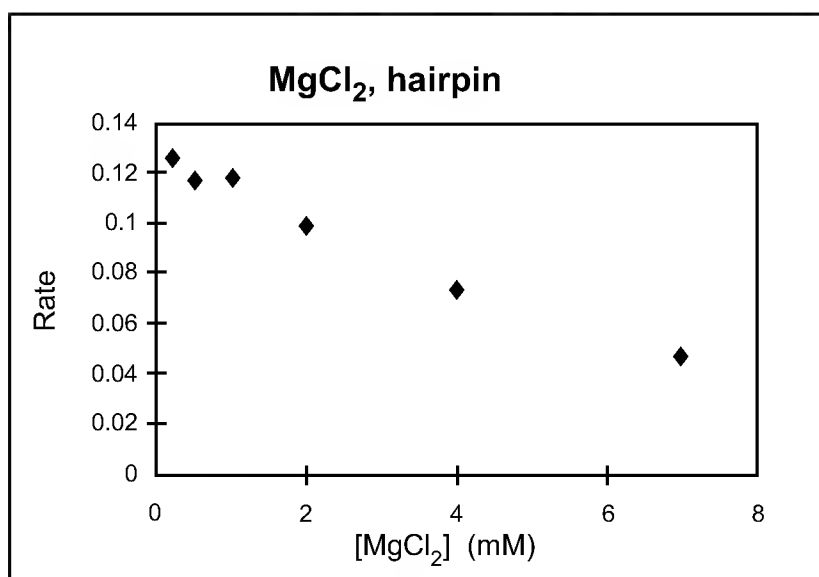


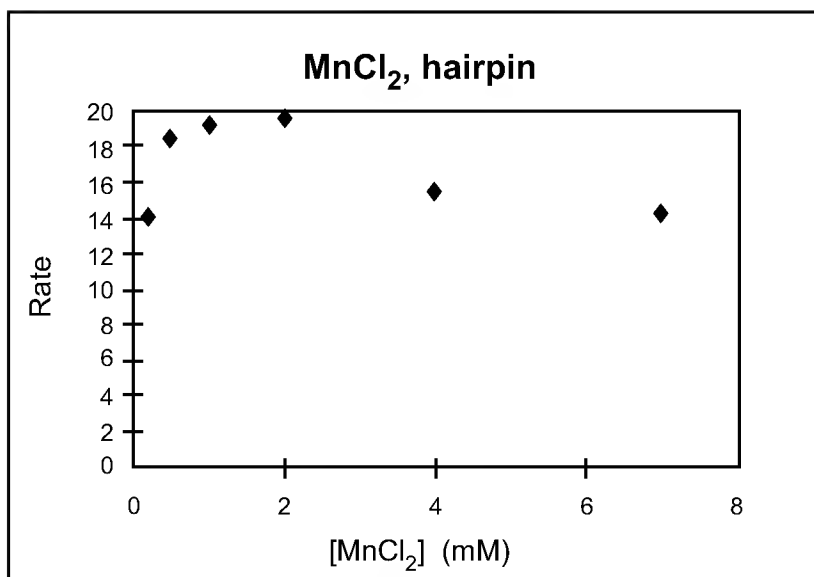
**FIG. 100C**

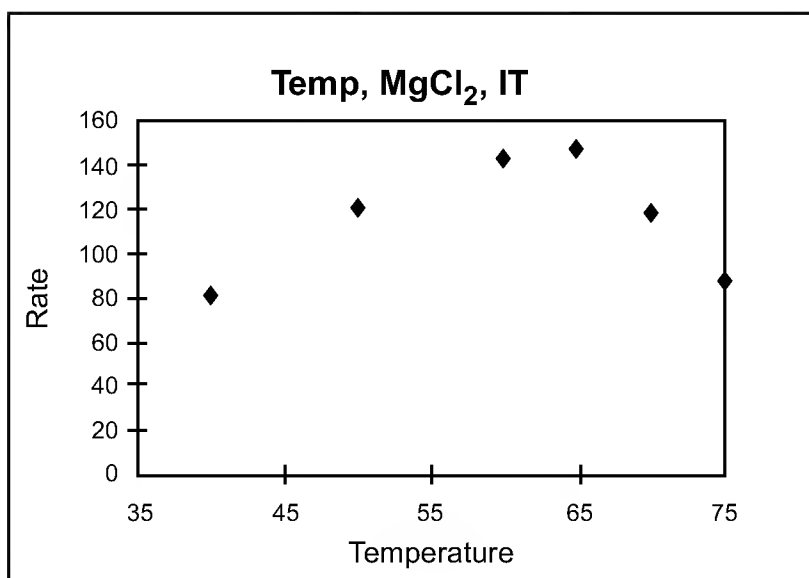
**FIG. 100D**

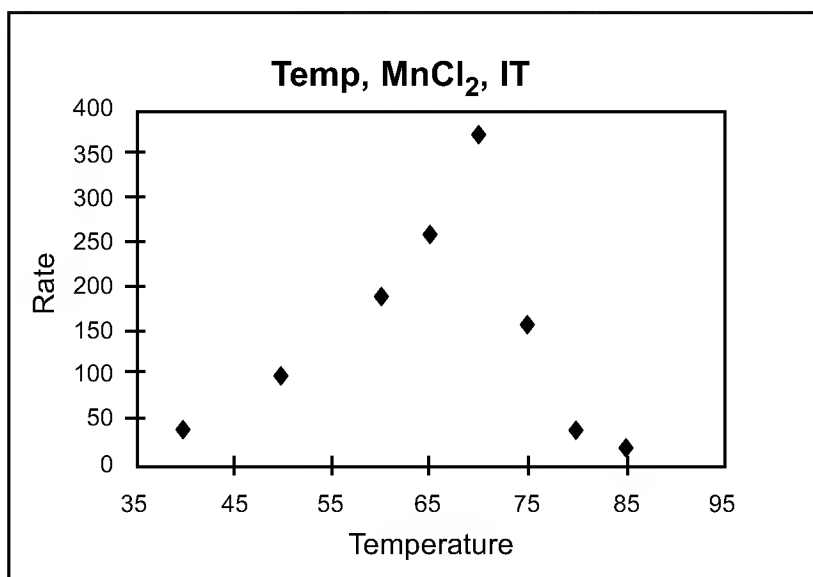
**FIG. 100E**

**FIG. 100F**

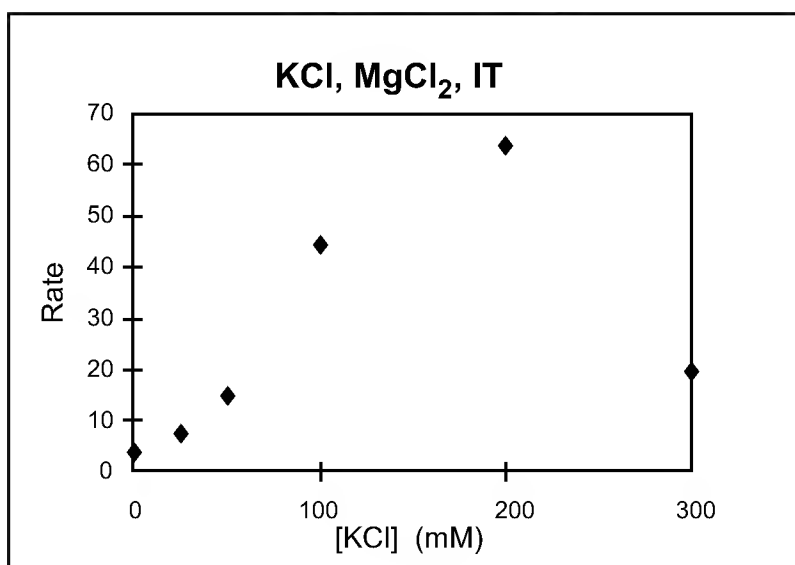
**FIG. 100G**

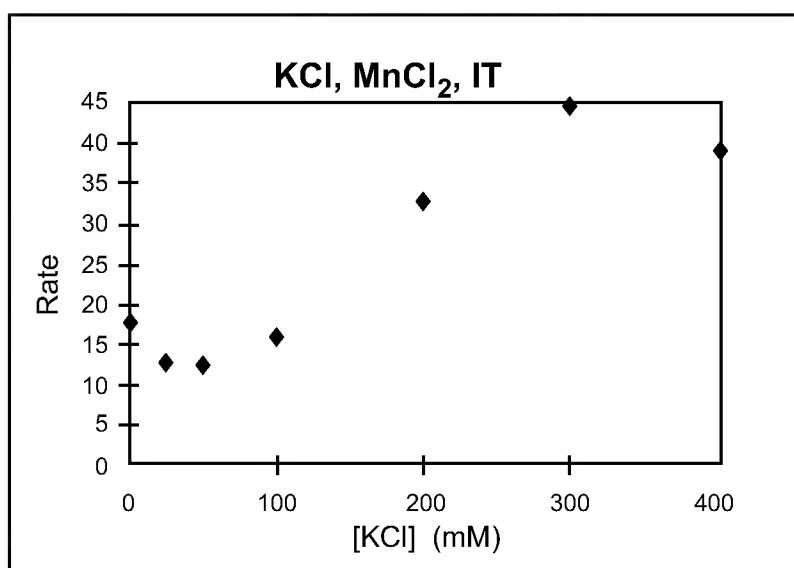
**FIG. 100H**

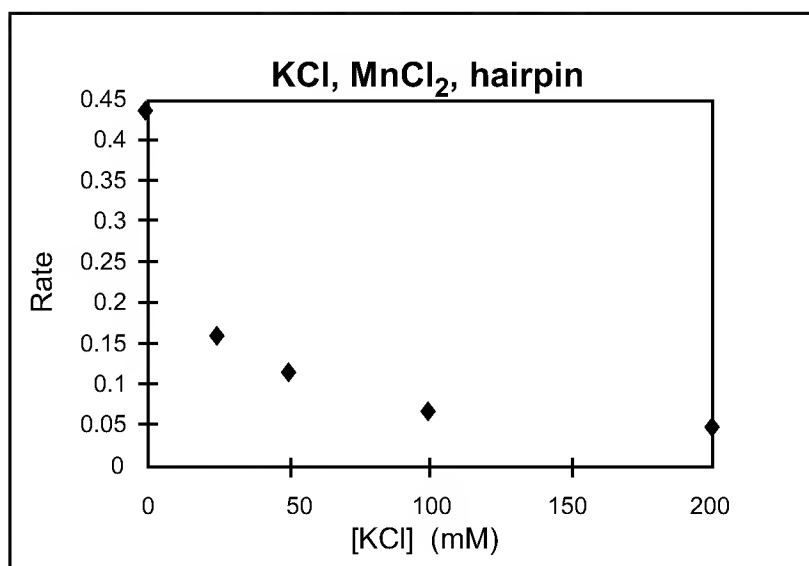
**FIG. 100I**

**FIG. 100J**



**FIG. 101A**

**FIG. 101B**

**FIG. 101D**

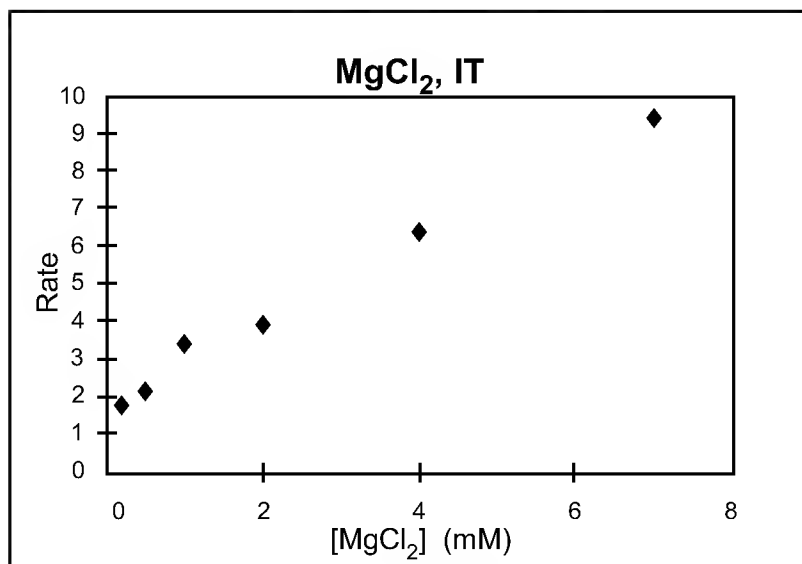
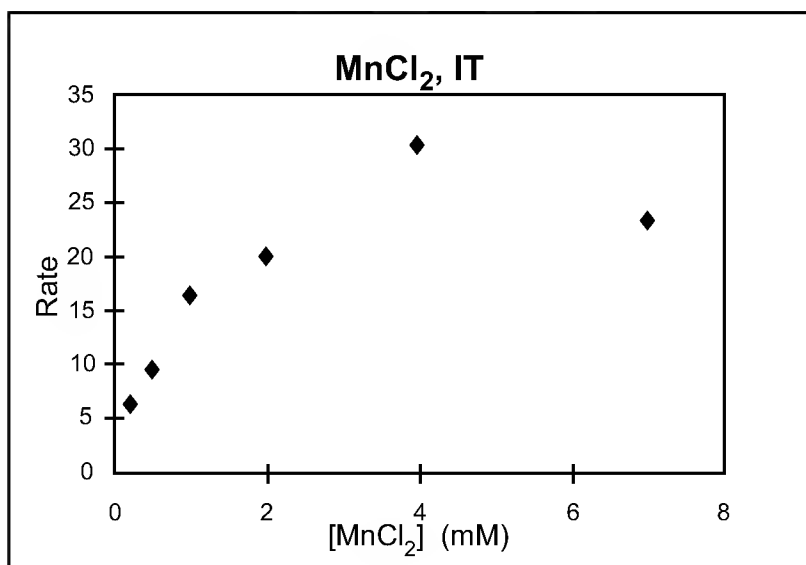
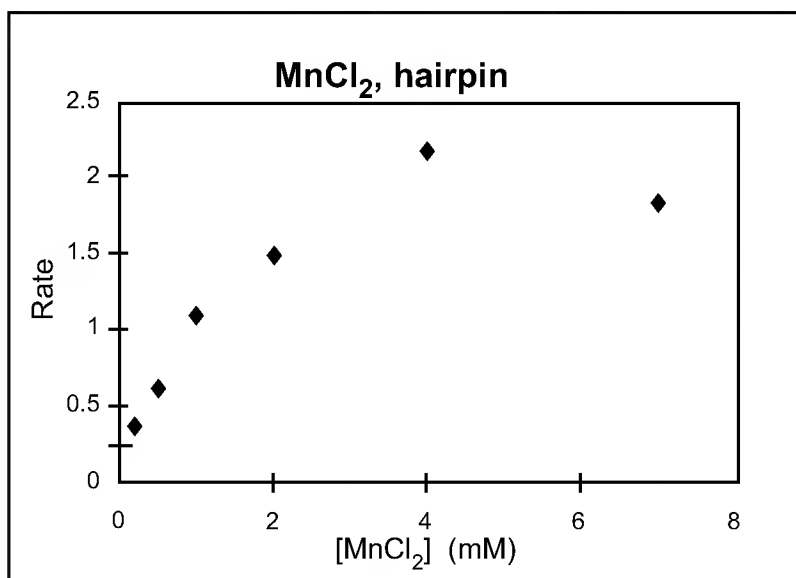
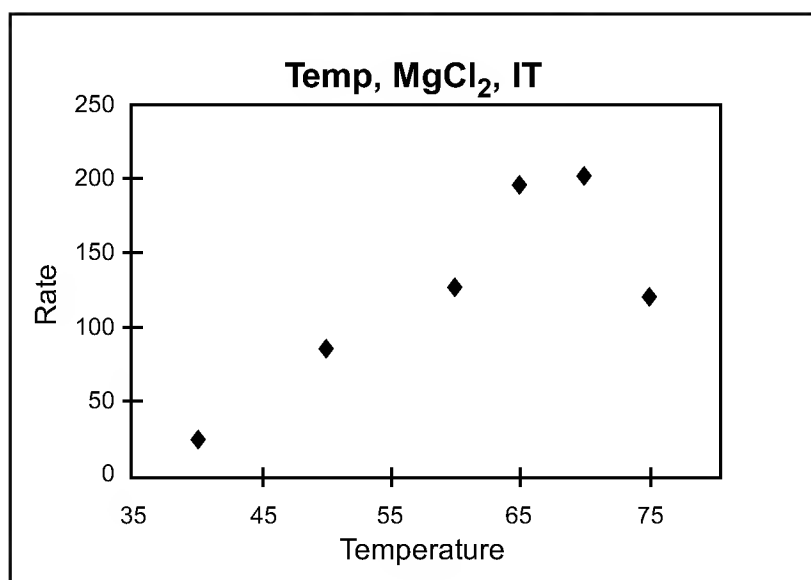
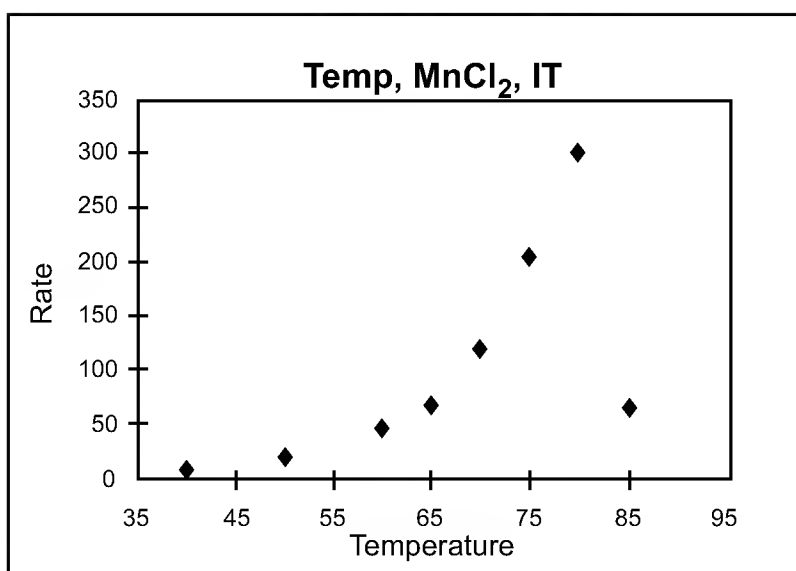
**FIG. 101E**

FIG. 101F

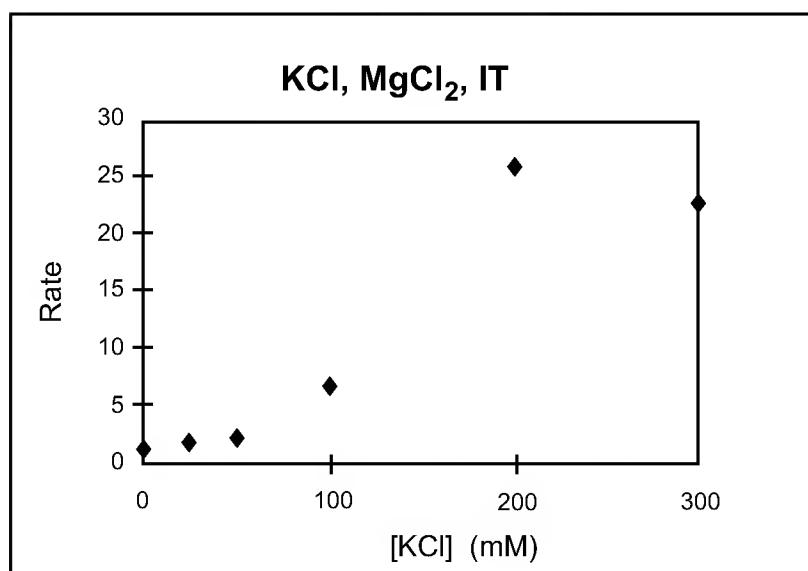


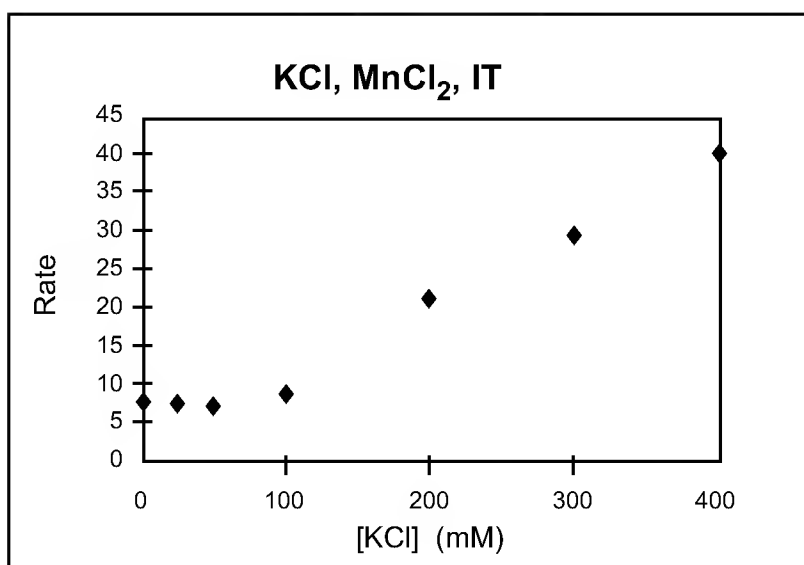
**FIG. 101H**

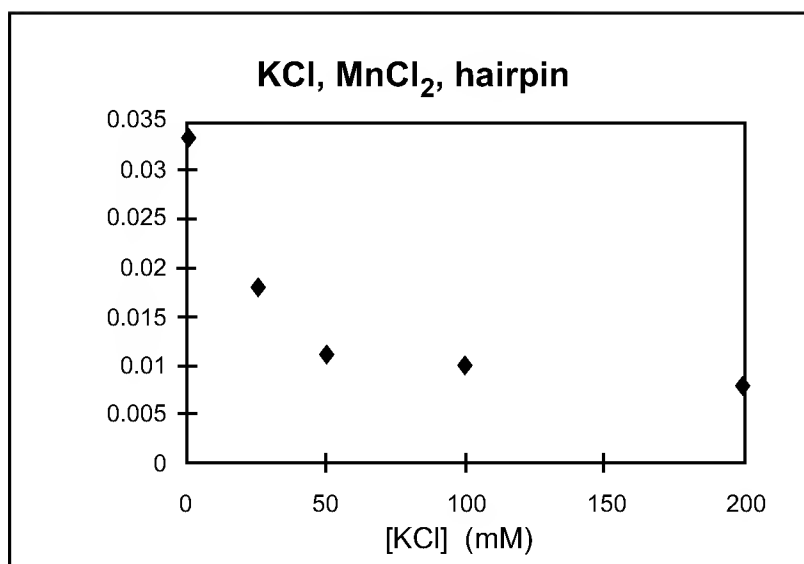
**FIG. 101I**

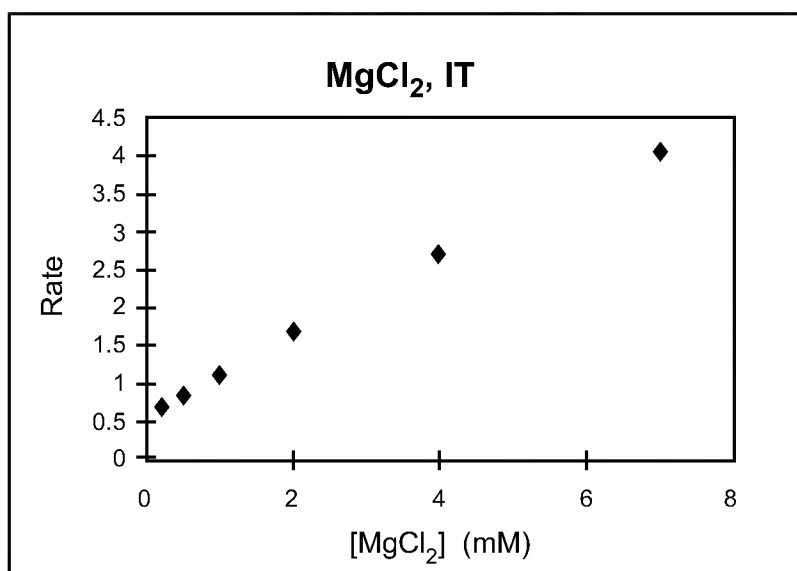
**FIG. 101J**

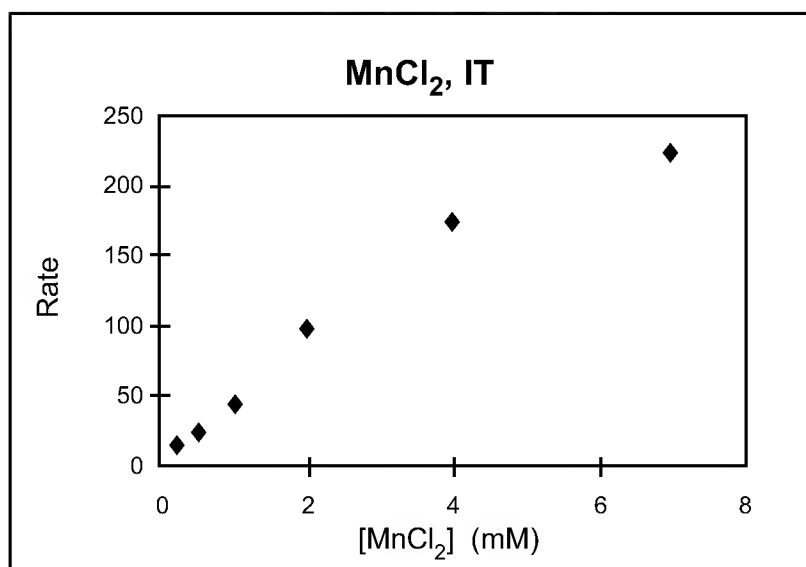


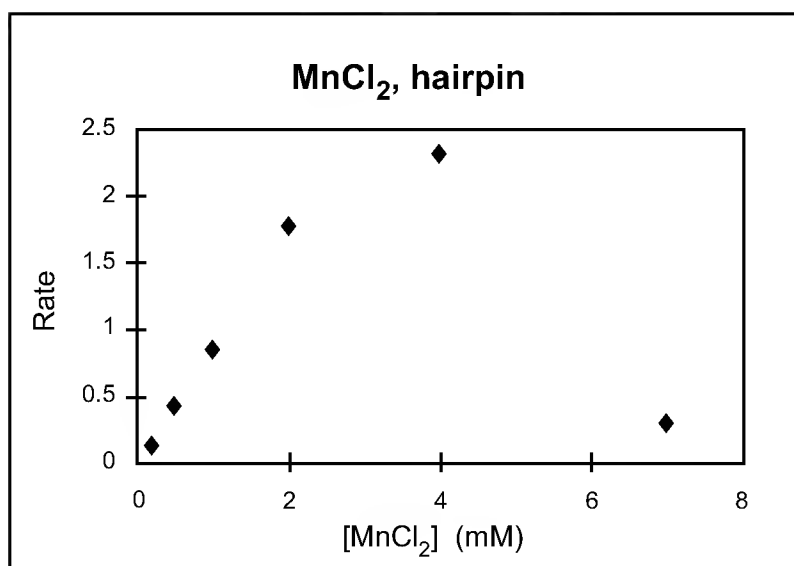
**FIG. 102A**

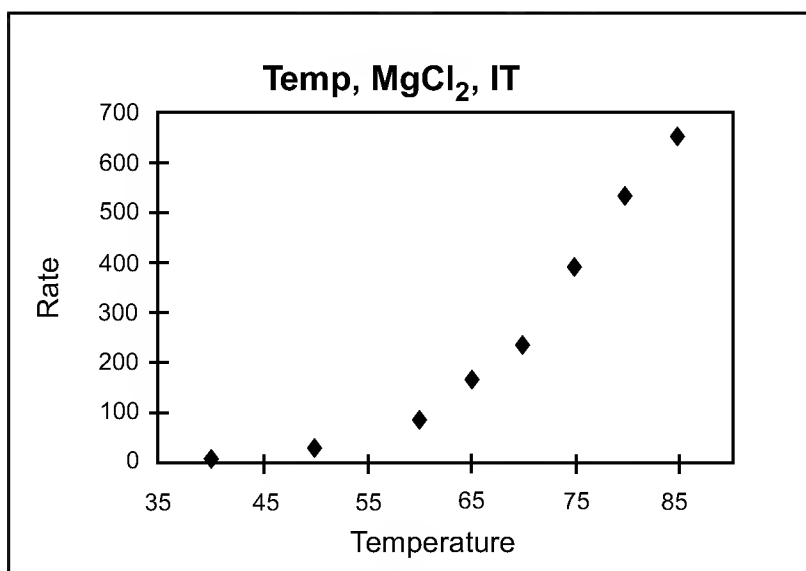
**FIG. 102B**

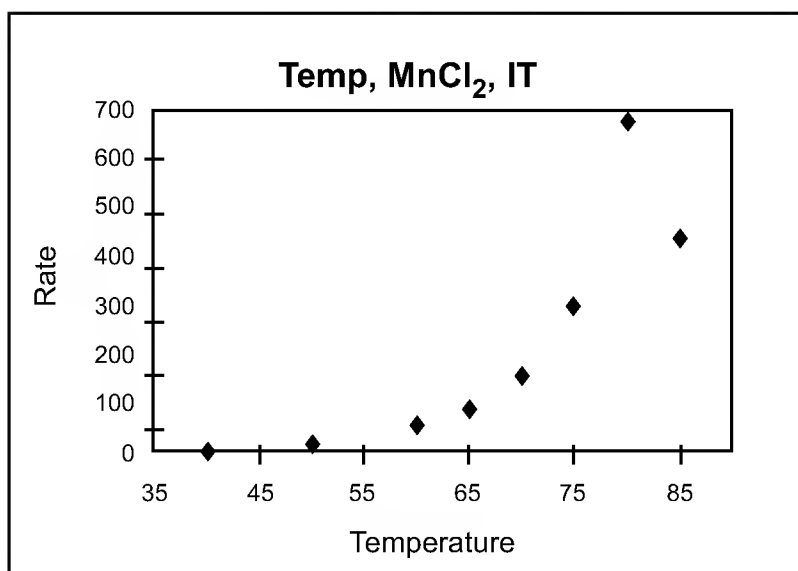
**FIG. 102D**

**FIG. 102E**

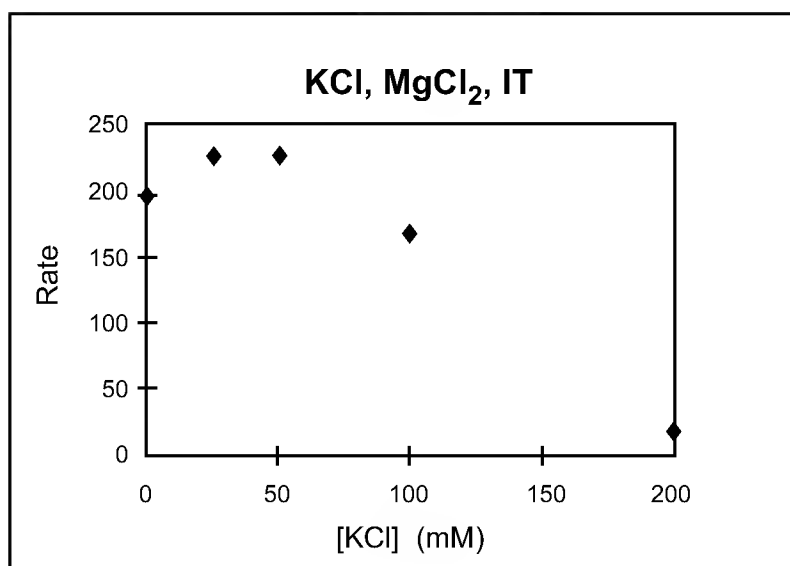
**FIG. 102F**

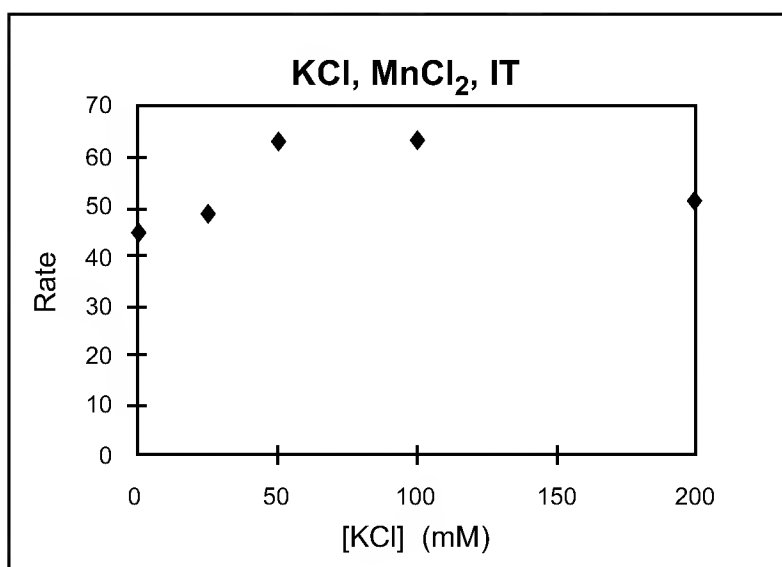
**FIG. 102H**

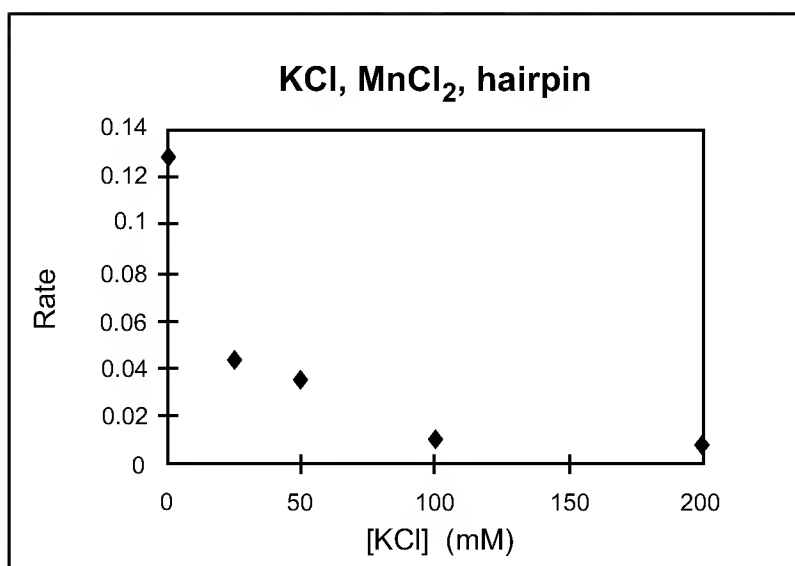
**FIG. 102I**

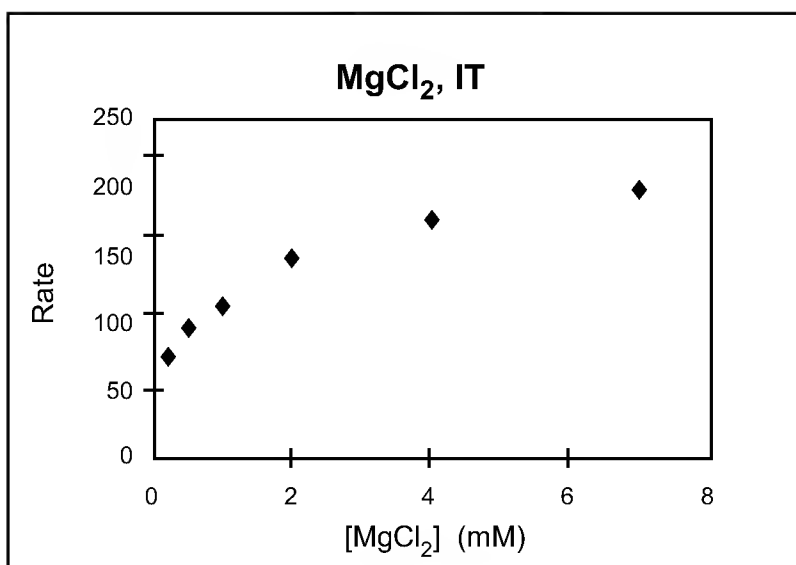
**FIG. 102J**

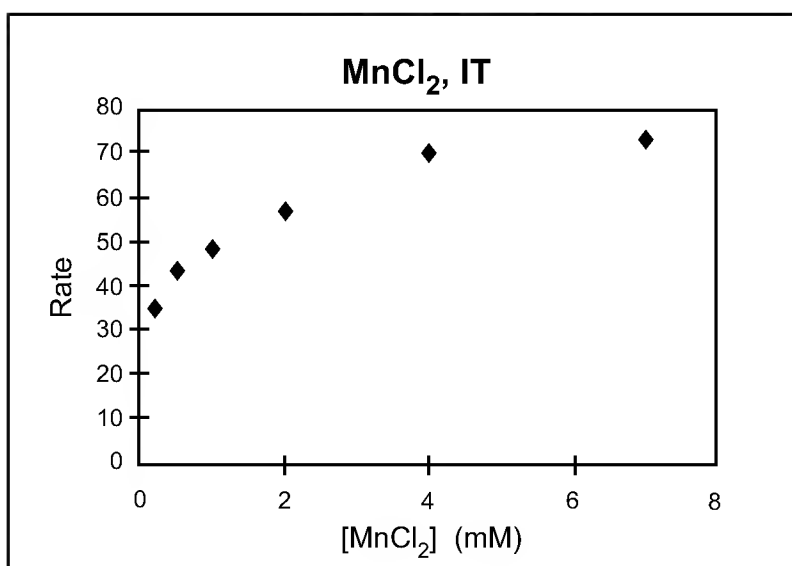


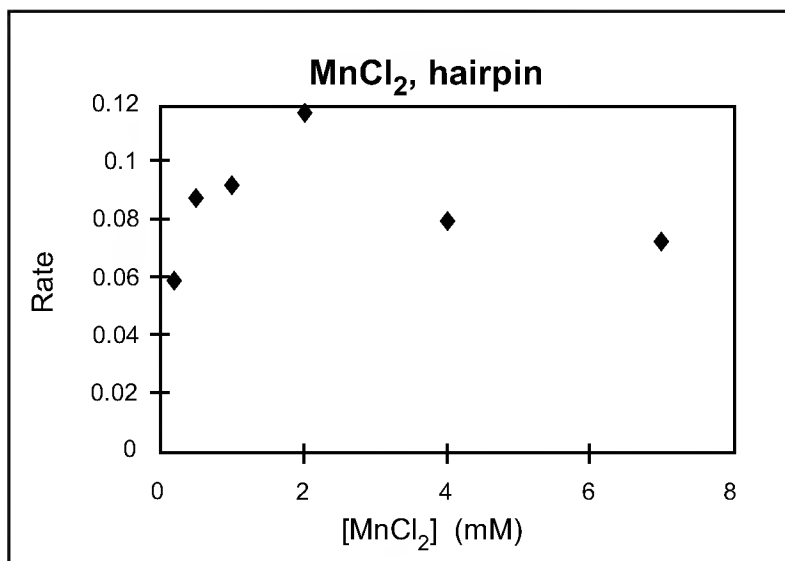
**FIG. 103A**

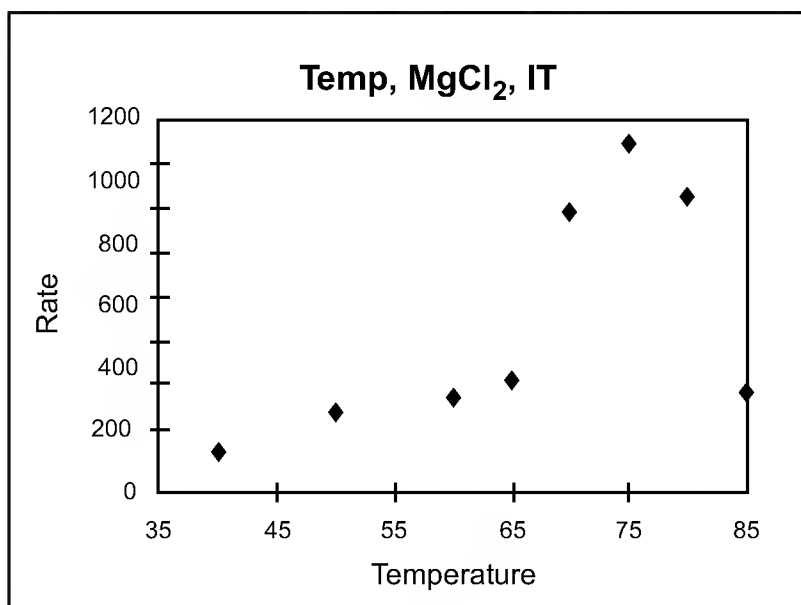
**FIG. 103B**

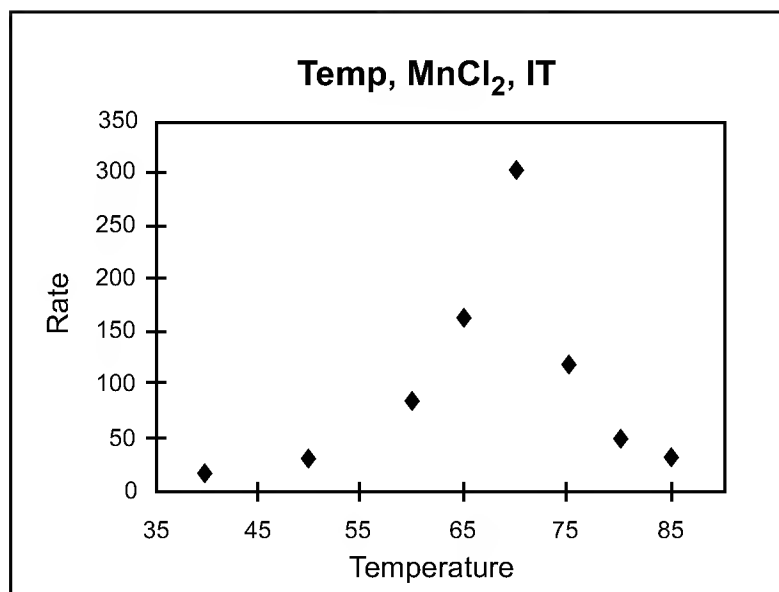
**FIG. 103D**

**FIG. 103E**

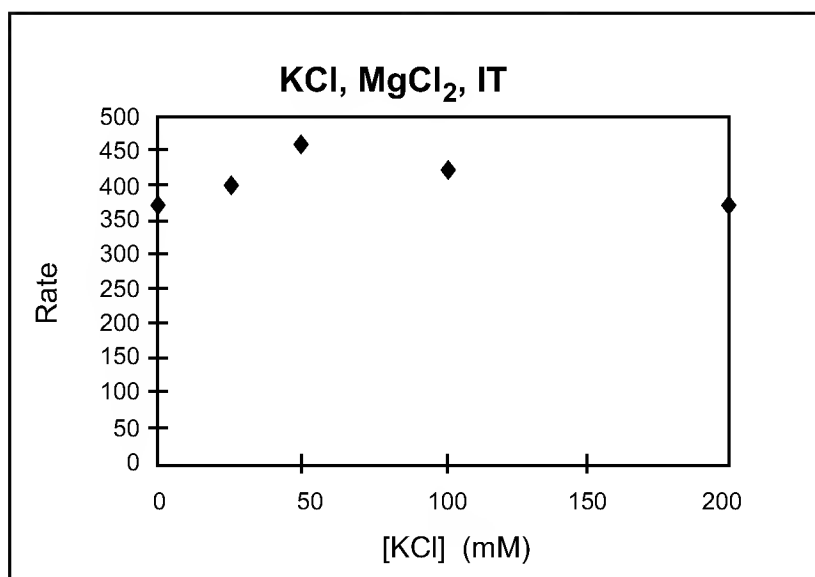
**FIG. 103F**

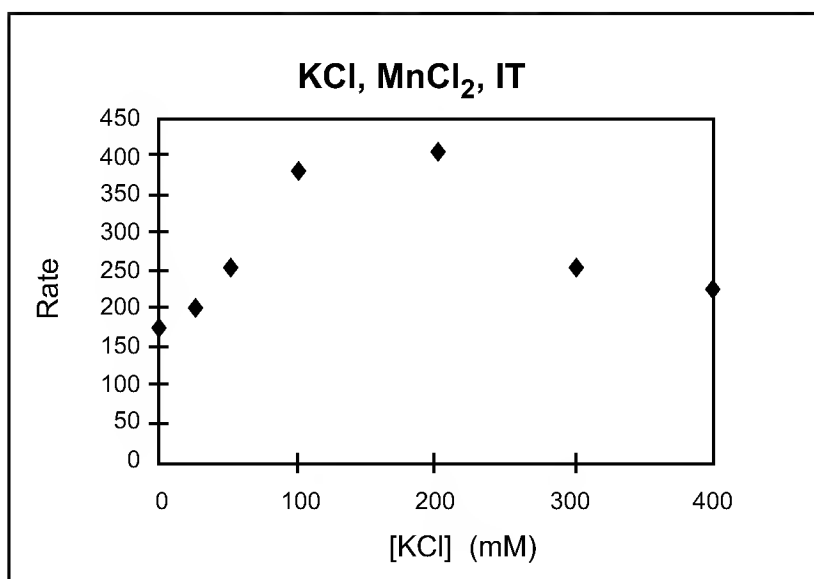
**FIG. 103H**

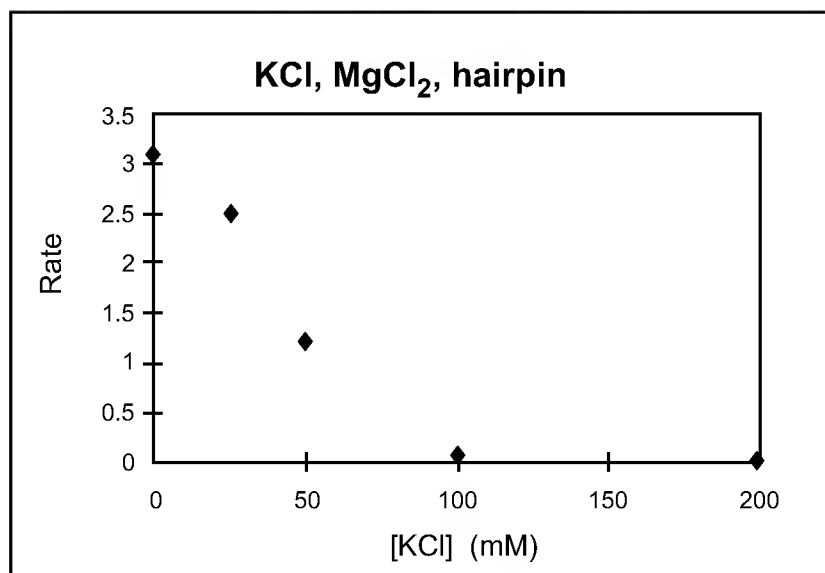
**FIG. 103I**

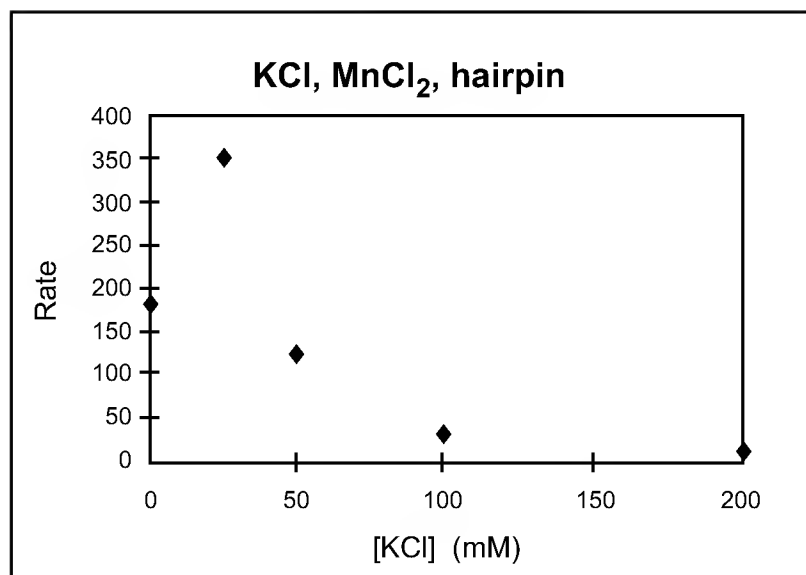
**FIG. 103J**

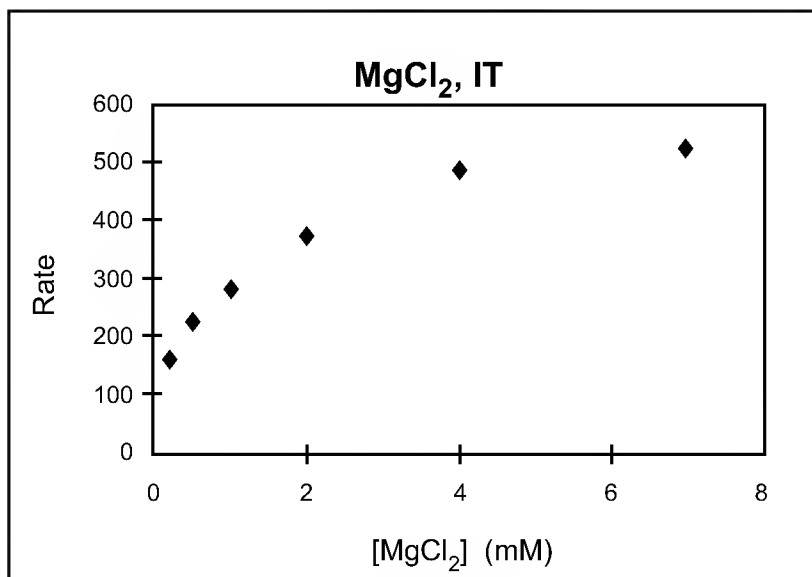


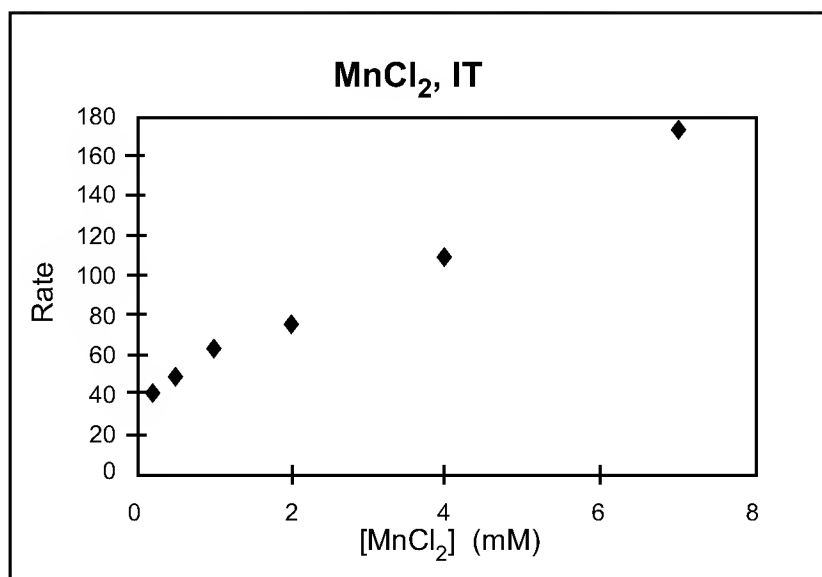
**FIG. 104A**

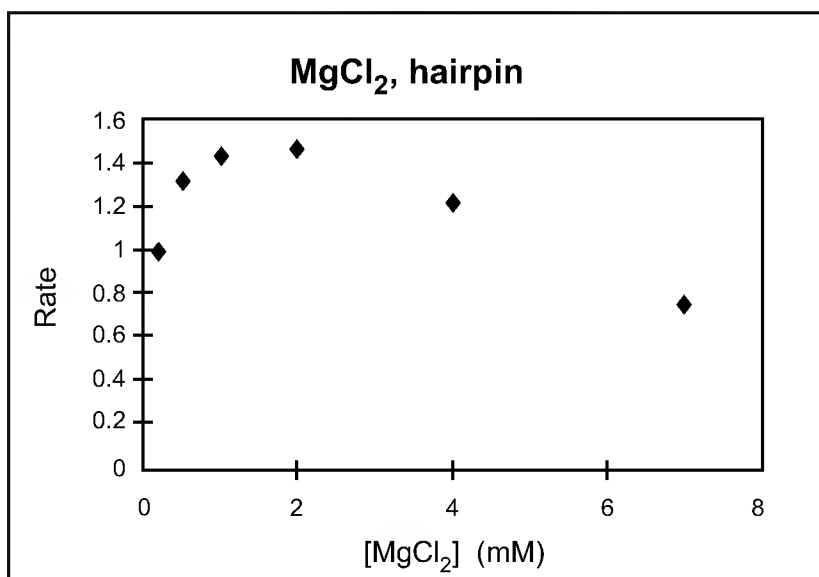
**FIG. 104B**

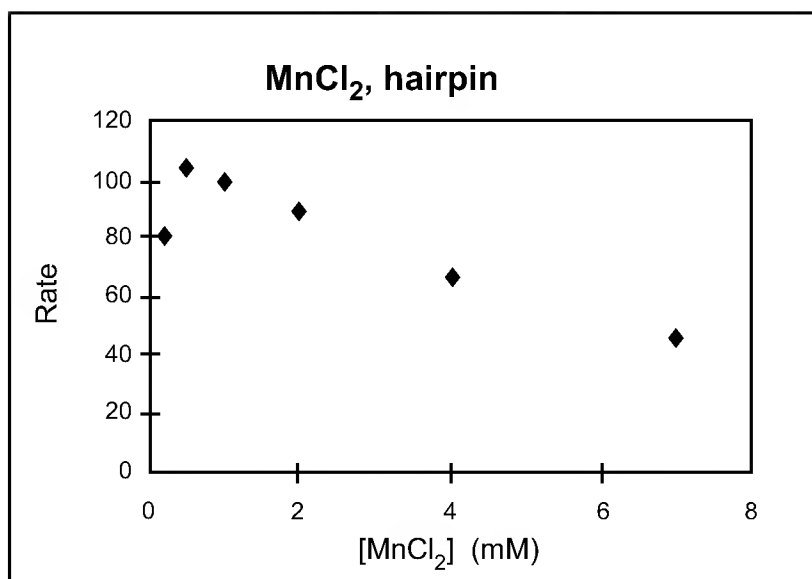
**FIG. 104C**

**FIG. 104D**

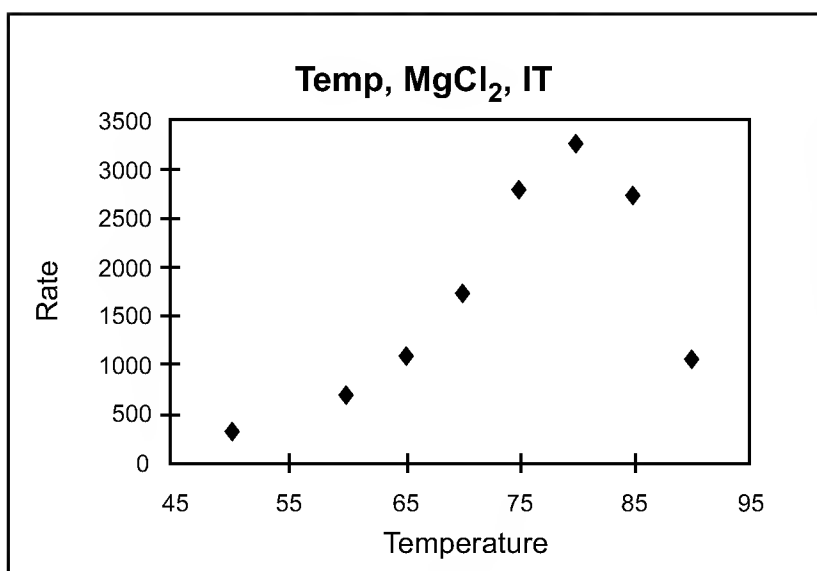
**FIG. 104E**

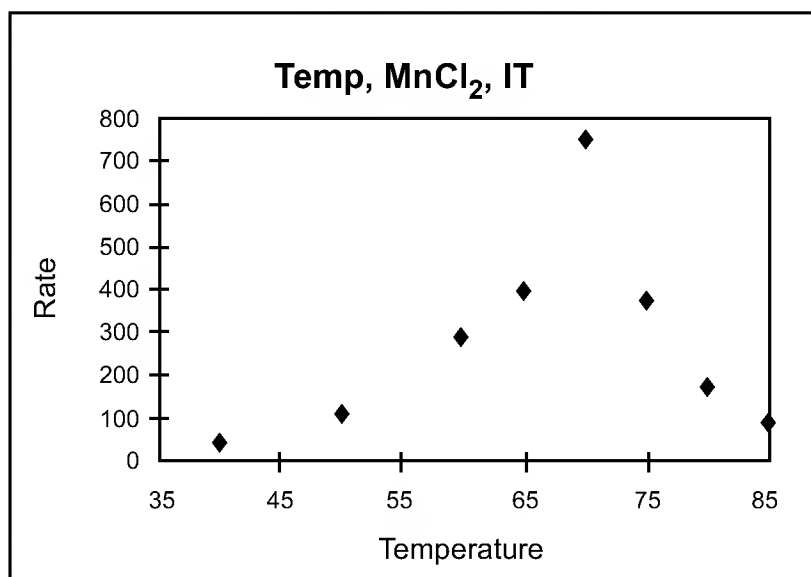
**FIG. 104F**

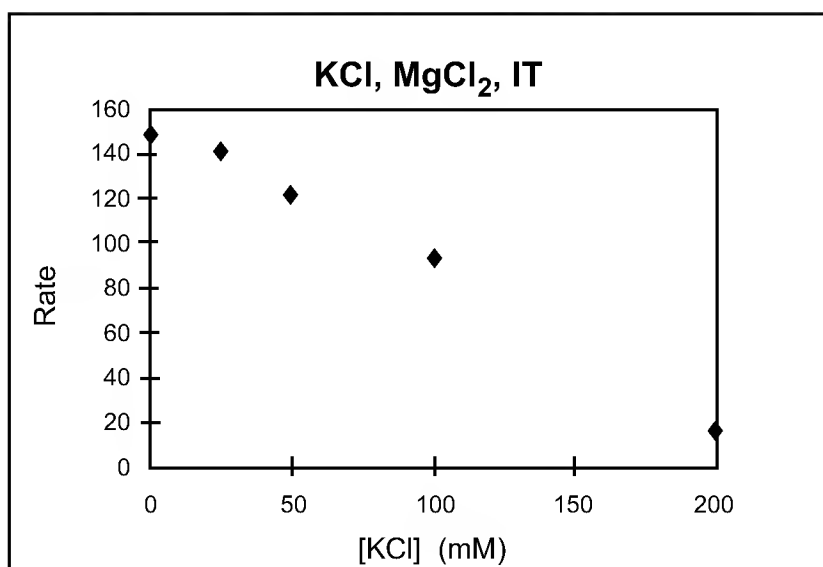
**FIG. 104G**

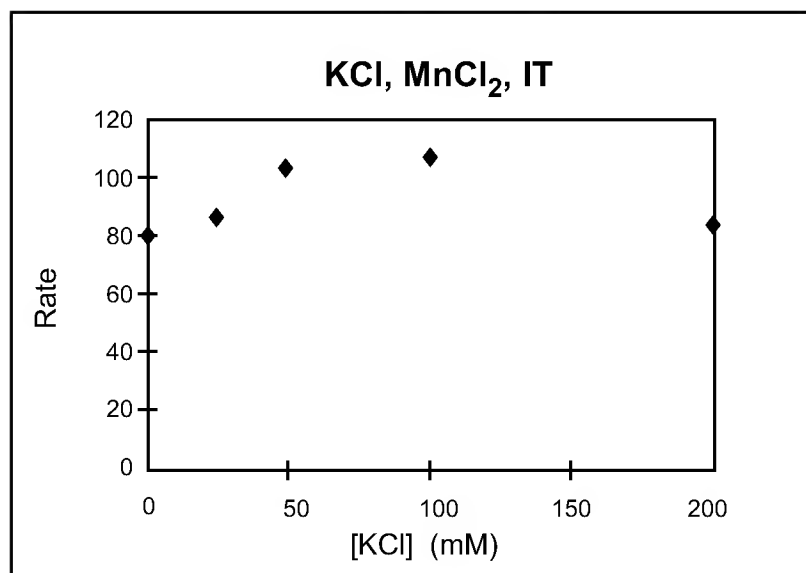
**FIG. 104H**

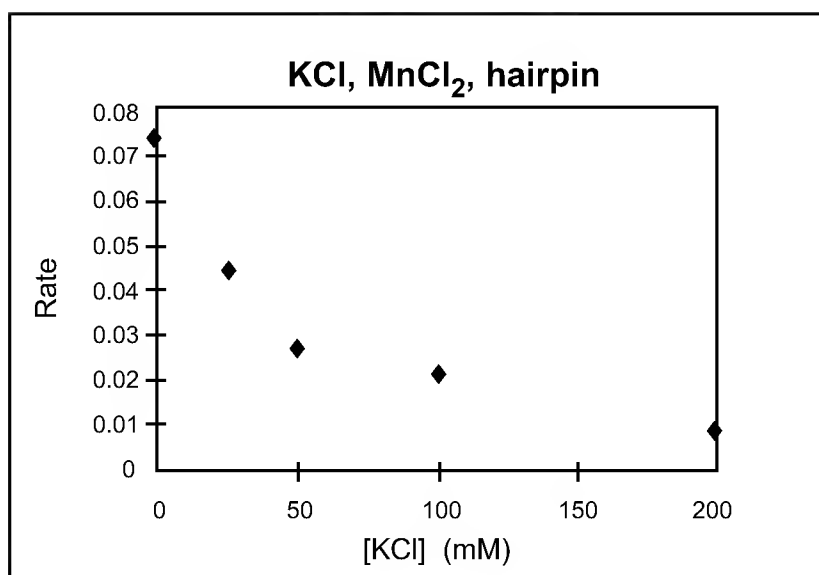


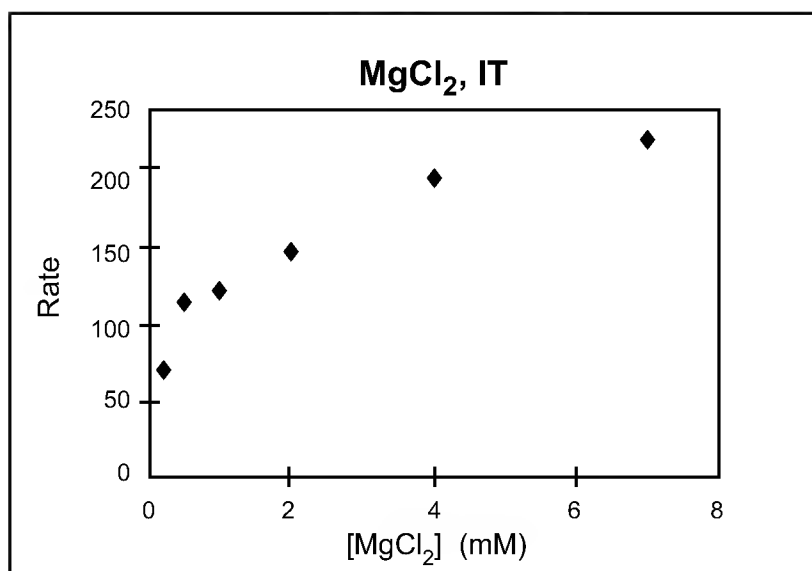
**FIG. 104I**

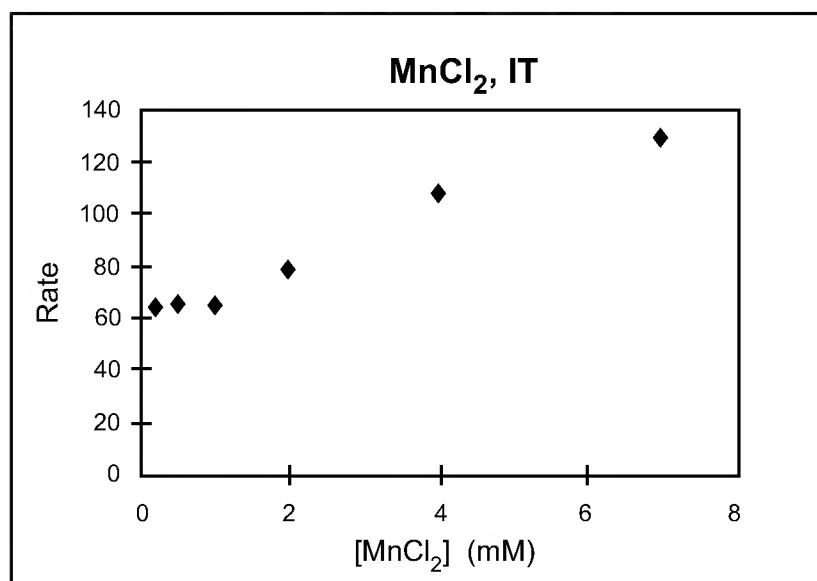
**FIG. 104J**

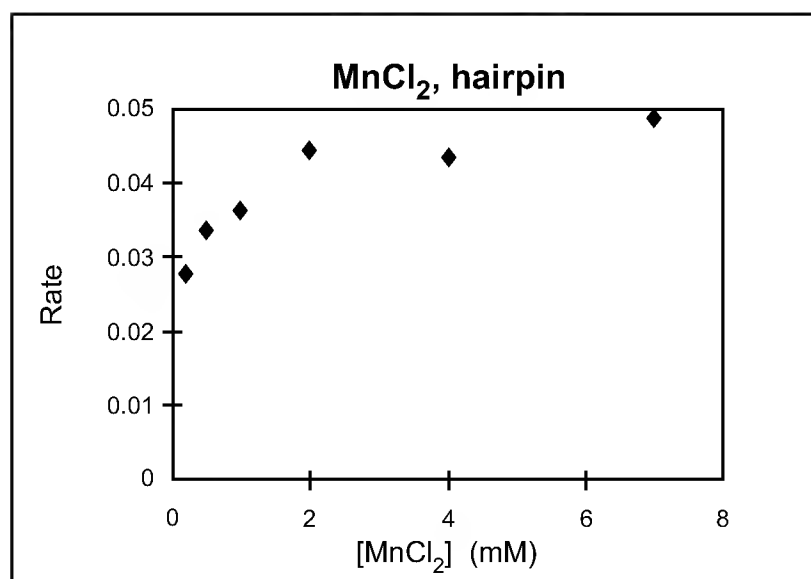
**FIG. 105A**

**FIG. 105B**

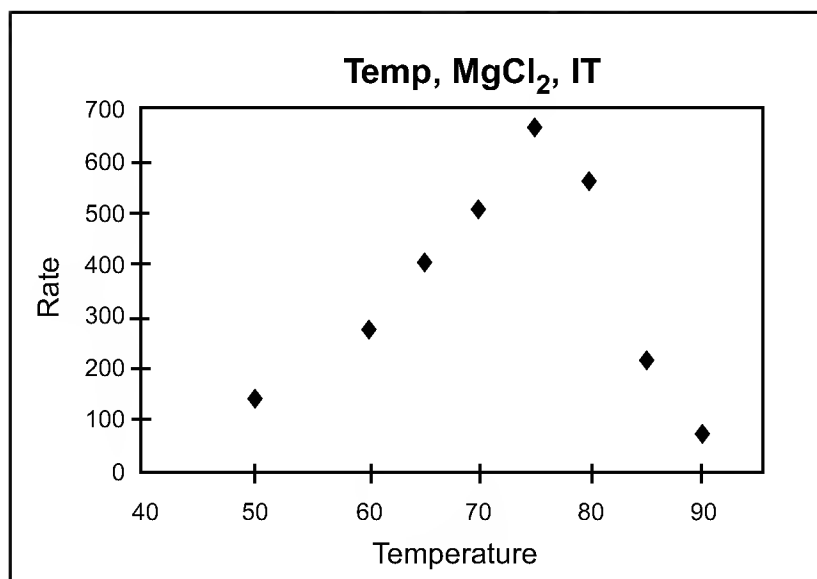
**FIG. 105D**

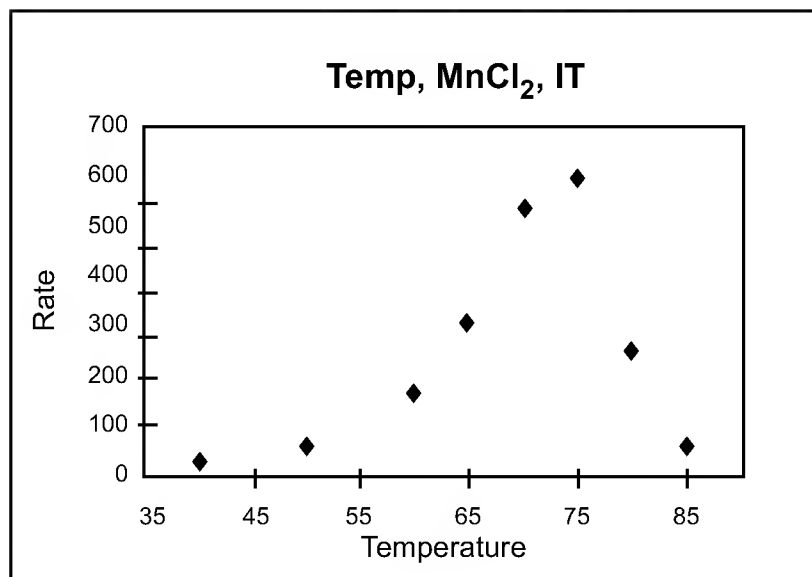
**FIG. 105E**

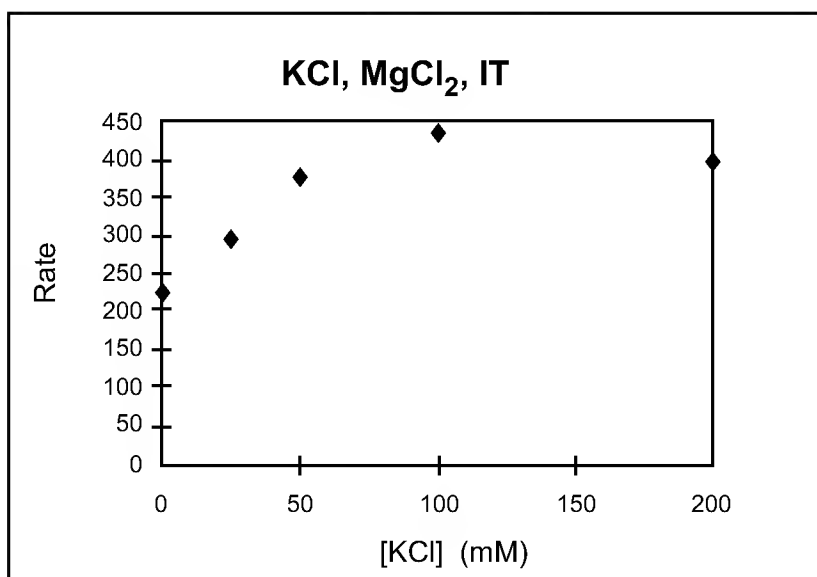
**FIG. 105F**

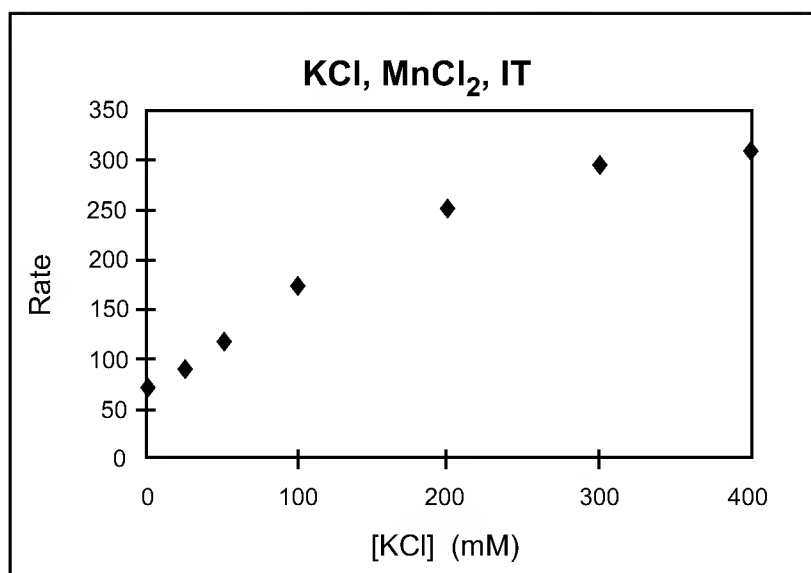
**FIG. 105H**

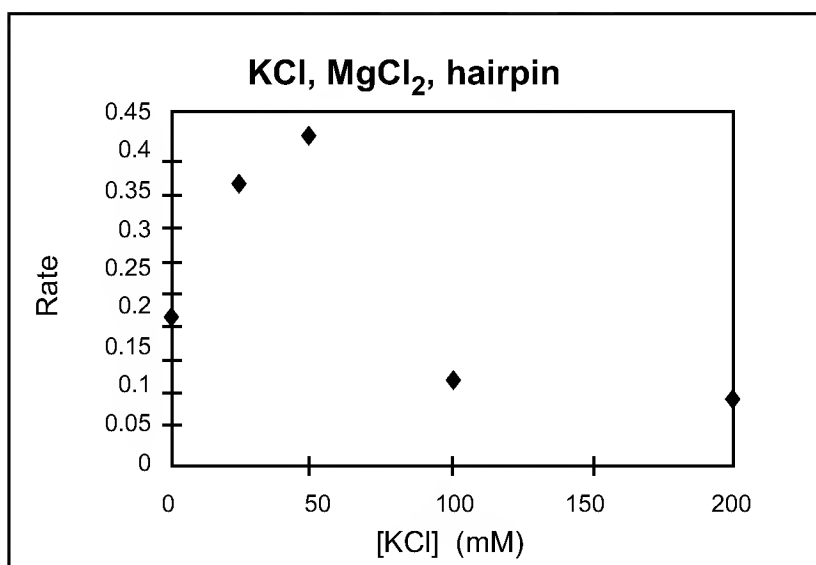


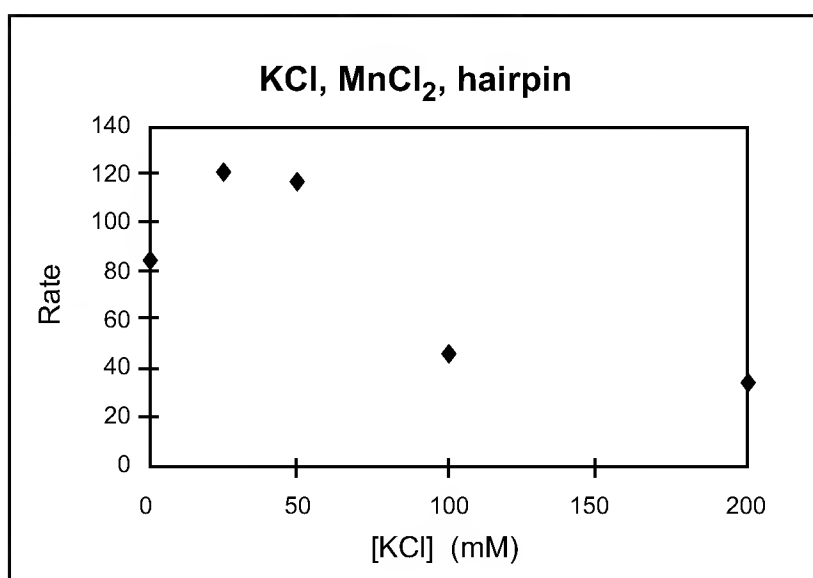
**FIG. 105I**

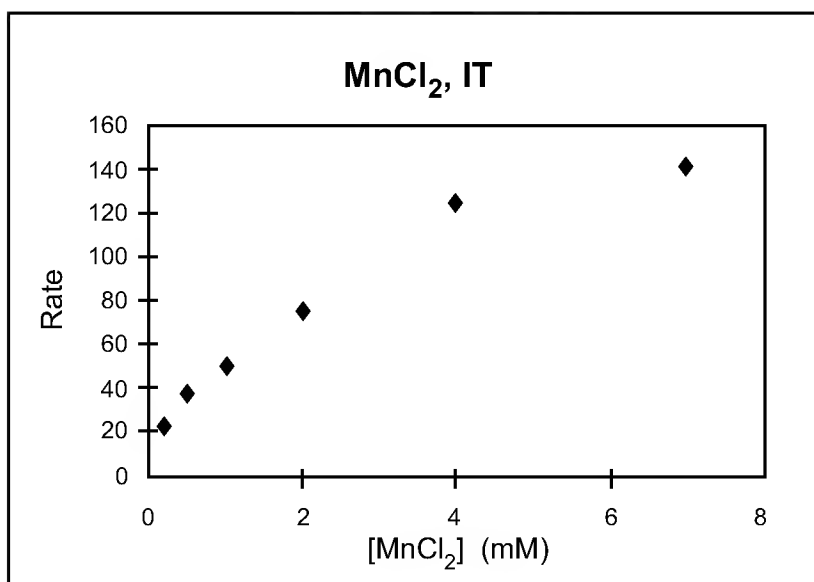
**FIG. 105J**

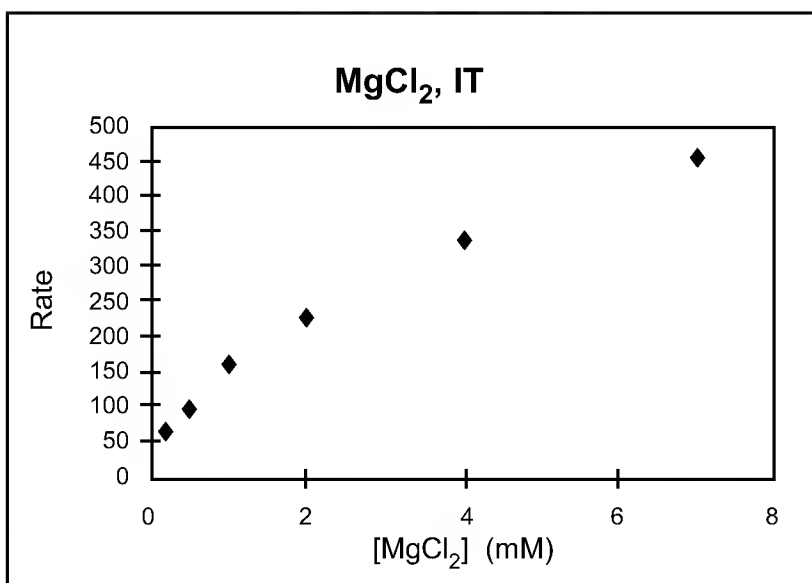
**FIG. 106A**

**FIG. 106B**

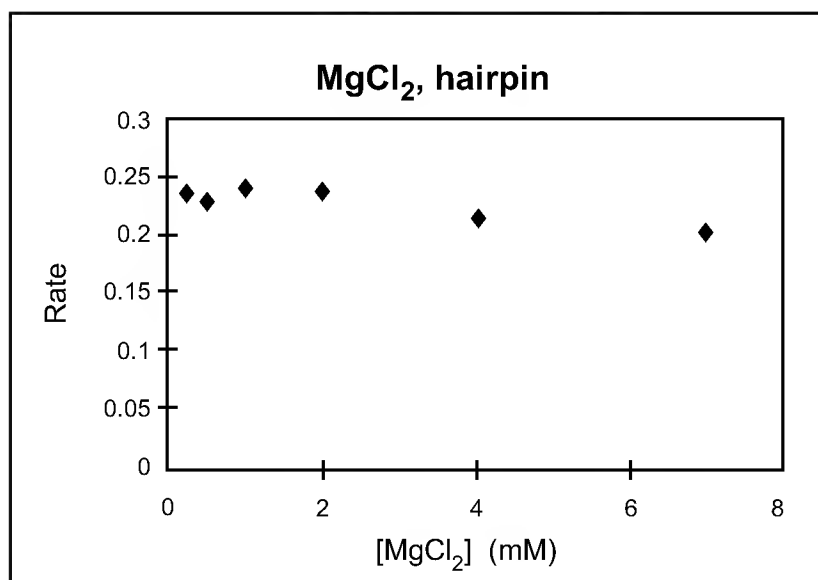
**FIG. 106C**

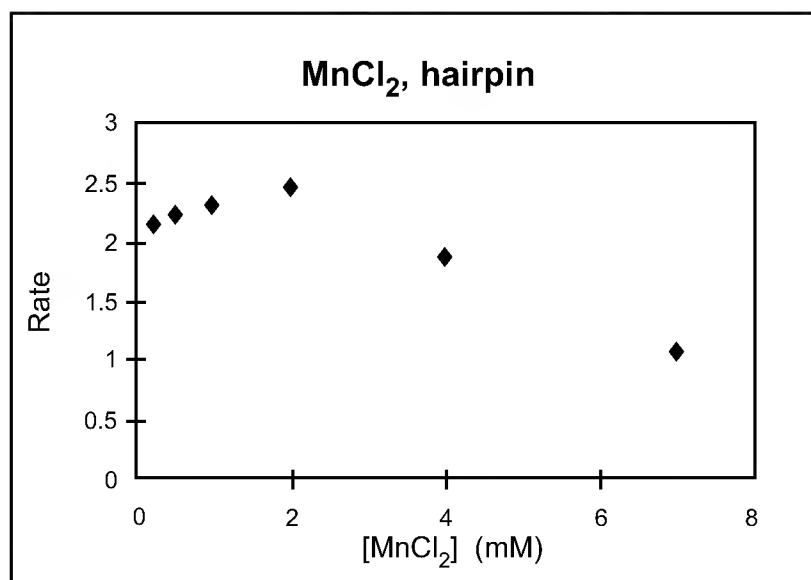
**FIG. 106D**

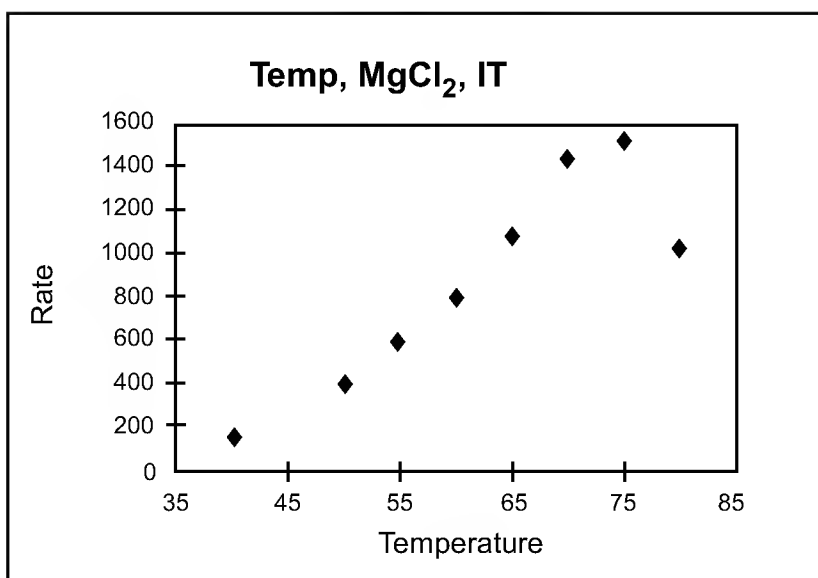
**FIG. 106E**

**FIG. 106F**



**FIG. 106G**

**FIG. 106H**

**FIG. 106I**

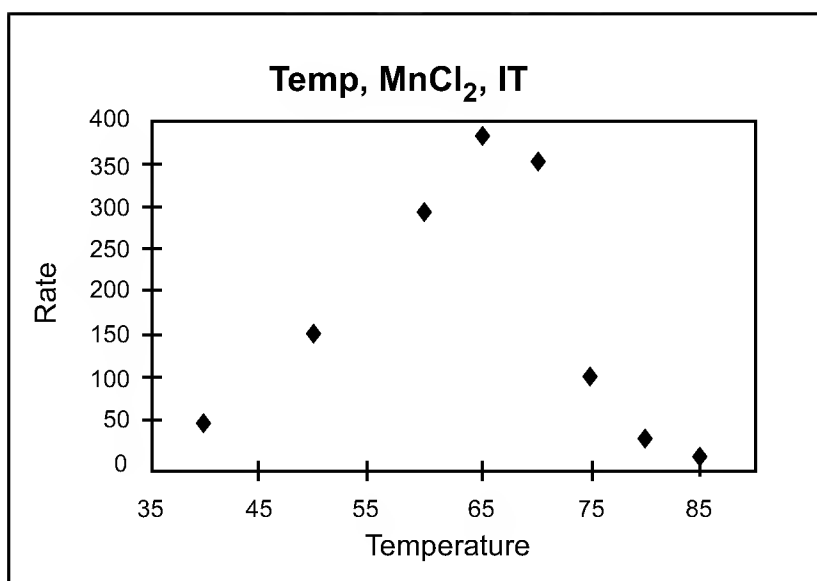
**FIG. 106J**

FIGURE 107

